

OM protein - protein search, using sw model

Run on: December 30, 2003, 12:21:17 ; Search time 10.5714 Seconds
 (without alignments)
 16.010 Million cell updates/sec

Title: US-10-033-526-1
 Perfect score: 4
 Sequence: 1 AAPF 4

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 36631

Minimum DB seq length: 4

Maximum DB seq length: 6

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	4	100.0	4	1	US-07-973-335-1	Sequence 1, Appli
2	4	100.0	4	1	US-08-155-331-19	Sequence 19, Appl
3	4	100.0	4	1	US-08-004-643C-2	Sequence 2, Appli
4	4	100.0	4	1	US-08-462-456-5	Sequence 5, Appli
5	4	100.0	4	1	US-08-282-860-1	Sequence 1, Appli
6	4	100.0	4	1	US-08-407-000-6	Sequence 6, Appli
7	4	100.0	4	1	US-07-890-422B-28	Sequence 28, Appl
8	4	100.0	4	1	US-08-276-936A-2	Sequence 2, Appli
9	4	100.0	4	1	US-08-345-820B-2	Sequence 2, Appli
10	4	100.0	4	1	US-08-544-143A-3	Sequence 3, Appli
11	4	100.0	4	1	US-08-397-602A-9	Sequence 9, Appli

12	4	100.0	4	1	US-08-437-029-5	Sequence 5, Appli
13	4	100.0	4	1	US-08-424-022-19	Sequence 19, Appl
14	4	100.0	4	1	US-08-439-534-10	Sequence 10, Appl
15	4	100.0	4	1	US-08-434-959-3	Sequence 3, Appli
16	4	100.0	4	1	US-08-434-959-4	Sequence 4, Appli
17	4	100.0	4	1	US-08-434-959-5	Sequence 5, Appli
18	4	100.0	4	1	US-08-434-959-6	Sequence 6, Appli
19	4	100.0	4	1	US-08-460-343B-56	Sequence 56, Appl
20	4	100.0	4	1	US-08-067-180B-2	Sequence 2, Appli
21	4	100.0	4	1	US-08-398-028B-56	Sequence 56, Appl
22	4	100.0	4	1	US-08-470-837-3	Sequence 3, Appli
23	4	100.0	4	2	US-08-722-268-2	Sequence 2, Appli
24	4	100.0	4	2	US-08-504-265B-56	Sequence 56, Appl
25	4	100.0	4	2	US-08-439-005-10	Sequence 10, Appl
26	4	100.0	4	2	US-08-698-575E-2	Sequence 2, Appli
27	4	100.0	4	2	US-08-424-017B-19	Sequence 19, Appl
28	4	100.0	4	2	US-08-751-070B-4	Sequence 4, Appli
29	4	100.0	4	3	US-09-069-823-2	Sequence 2, Appli
30	4	100.0	4	3	US-09-076-460-1	Sequence 1, Appli
31	4	100.0	4	3	US-08-950-618-3	Sequence 3, Appli
32	4	100.0	4	3	US-08-950-618-18	Sequence 18, Appl
33	4	100.0	4	3	US-08-950-618-31	Sequence 31, Appl
34	4	100.0	4	3	US-09-120-365-101	Sequence 101, App
35	4	100.0	4	3	US-08-319-501-10	Sequence 10, Appl
36	4	100.0	4	3	US-09-168-010-3	Sequence 3, Appli
37	4	100.0	4	3	US-09-168-010-18	Sequence 18, Appl
38	4	100.0	4	3	US-09-168-010-31	Sequence 31, Appl
39	4	100.0	4	3	US-08-905-359A-25	Sequence 25, Appl
40	4	100.0	4	3	US-09-353-556-25	Sequence 25, Appl
41	4	100.0	4	3	US-09-515-039-101	Sequence 101, App
42	4	100.0	4	3	US-09-147-502A-1	Sequence 1, Appli
43	4	100.0	4	3	US-09-326-039-15	Sequence 15, Appl
44	4	100.0	4	4	US-09-343-650-3	Sequence 3, Appli
45	4	100.0	4	4	US-09-343-650-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1

US-07-973-335-1

; Sequence 1, Application US/07973335

; Patent No. 5338547

; GENERAL INFORMATION:

; APPLICANT: Kennedy and Szuhaj

; TITLE OF INVENTION: No. 5338547e1 Bowman-Birk Inhibitor

; TITLE OF INVENTION: Product For Use As An Anticarcinogenesis Agent

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz

; ADDRESSEE: Mackiewicz & No. 5338547ris

; STREET: One Liberty Place - 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/973,335
; FILING DATE: 19921102
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 824,719
; FILING DATE: January 17, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 579,155
; FILING DATE: September 6, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: UPSC-0003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-973-335-1

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Query Match          100.0%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      1 AAPF 4
        ||||
Db      1 AAPF 4

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RESULT 2

US-08-155-331-19

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; Sequence 19, Application US/08155331
; Patent No. 5441931

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GENERAL INFORMATION:

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; APPLICANT: Foster, Donald C
; APPLICANT: Sprecher, Cindy
; APPLICANT: No. 5441931ris, Kjeld
; TITLE OF INVENTION: NOVEL HUMAN AMYLOID PROTEIN PRECURSOR
; TITLE OF INVENTION: HOMOLOG AND KUNITZ-TYPE INHIBITOR
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 4225 Roosevelt Way, N.E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/155,331
;      FILING DATE:
;      CLASSIFICATION:  435
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/985,692
;      FILING DATE:  02-DEC-1992
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Parker, Gary E
;      REGISTRATION NUMBER:  31-684
;      REFERENCE/DOCKET NUMBER:  92-21C1
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-547-8080 ext 322
;      TELEFAX:  206-548-2329
;      INFORMATION FOR SEQ ID NO:  19:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  peptide
;      FRAGMENT TYPE:  internal
;      FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  1..4
;      OTHER INFORMATION:  /label= ALA-1
;      OTHER INFORMATION:  /note= "Amino terminal alanine residue is capped
;      OTHER INFORMATION:  with a succinyl group"
;      FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  1..4
;      OTHER INFORMATION:  /label= Phe-4
;      OTHER INFORMATION:  /note= "Carboxyl-terminal phenylalanine residue is
;      OTHER INFORMATION:  capped with p-nitroanil..."
US-08-155-331-19

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Query Match          100.0%;  Score 4;  DB 1;  Length 4;
Best Local Similarity 100.0%;  Pred. No. 2.5e+05;
Matches      4;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

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Qy      1 AAPF 4
        ||||
Db      1 AAPF 4

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RESULT 3

US-08-004-643C-2

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; Sequence 2, Application US/08004643C
; Patent No. 5480779
; GENERAL INFORMATION:
; APPLICANT:  Gunter Fischer & Gerhard K llerz
; TITLE OF INVENTION:  Cyclosporine Assay
; NUMBER OF SEQUENCES:  7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Gunter Fischer et al. c/o G. P. Katona

```

```

; STREET: 230 Park Avenue, Room 2200
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10169
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM pc compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: conf. to Patentin Release #1.0, Ver.#1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/004,643C
; FILING DATE: 12 January 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 703,590
; FILING DATE: 20 May 1991
; APPLICATION NUMBER: 398,092
; FILING DATE: 24 August 1989
; APPLICATION NUMBER: DD WP 601 F/319 577W
; FILING DATE: 07 September 1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Katona, Gabriel P.
; REGISTRATION NUMBER: 20,829
; REFERENCE/DOCKET NUMBER: 691-003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)986-3377
; TELEFAX: (212)986-6126
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-004-643C-2

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Query Match          100.0%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

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Qy      1 AAPF 4
        ||||
Db      1 AAPF 4

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RESULT 4
US-08-462-456-5
; Sequence 5, Application US/08462456
; Patent No. 5510333
; GENERAL INFORMATION:
; APPLICANT: Angelastro, Michael R
; APPLICANT: Bey, Philippe
; APPLICANT: Doherty, Niall S
; APPLICANT: Janusz, Michael J
; APPLICANT: Mehdi, Shujaath
; APPLICANT: Peet, No. 5510333ton P

```

```

; TITLE OF INVENTION: Inhibitors of Cathepsin G and Elastase
; TITLE OF INVENTION: for Preventing Connective Tissue Degradation
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marion Merrell Dow Inc.
; STREET: 2110 East Galbraith Rd.
; CITY: Cincinnati P. O. Box 156300
; STATE: Ohio
; COUNTRY: USA
; ZIP: 45215-6300
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,456
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/342,999
; FILING DATE:
; APPLICATION NUMBER: US/08/222,552
; FILING DATE:
; APPLICATION NUMBER: US/07/987,587
; FILING DATE:
; APPLICATION NUMBER: US/07/704,499
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Nesbitt, Stephen L
; REGISTRATION NUMBER: 28,981
; REFERENCE/DOCKET NUMBER: M01593
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (513) 948-7965
; TELEFAX: (513) 948-7961
; TELEX: 214320
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-462-456-5

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Query Match          100.0%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      1 AAPF 4
        ||||
Db      1 AAPF 4

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RESULT 5
US-08-282-860-1
; Sequence 1, Application US/08282860
; Patent No. 5561108

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; GENERAL INFORMATION:
; APPLICANT: Tsay, Grace C.
; APPLICANT: Cheung, Neal K. H.
; APPLICANT: Bettencourt, Jeffrey D.
; TITLE OF INVENTION: Preparation of Alpha-1 Antichymotrypsin
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 800 Dwight Way
; STREET: P. O. Box 1986
; CITY: Berkeley
; STATE: California
; COUNTRY: USA
; ZIP: 94701-1986
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb Storage
; COMPUTER: IBM
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/282,860
; FILING DATE: 07/29/94
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gibling, James A.
; REGISTRATION NUMBER: 25772
; REFERENCE/DOCKET NUMBER: MSB-7214
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510)705-7910
; TELEFAX: (510)705-7904
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4
; TYPE: amino acid
; STRANDEDNESS: single strand
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: peptide
; FEATURE:
; NAME/KEY: Modified peptide used for enzyme activity assay
; OTHER INFORMATION: Peptide is modified with n-terminal
; OTHER INFORMATION: succinyl group and c-terminal p-nitroanilide group
; PUBLICATION INFORMATION:
; AUTHORS: Del Mar, E. G.
; AUTHORS: Largman, C.
; AUTHORS: Broderick, J. W.
; TITLE: A Sensitive New Substrate for Chymotrypsin
; JOURNAL: Analytical Biochemistry
; VOLUME: 99
; PAGES: 316-329
; DATE: 01-NOV-1979
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 4
US-08-282-860-1

Query Match 100.0%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
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Db 1 AAPF 4

RESULT 6

US-08-407-000-6

; Sequence 6, Application US/08407000
; Patent No. 5578324

; GENERAL INFORMATION:

; APPLICANT: Dohi, Masahiko
; APPLICANT: Nishibe, Yoshihisa
; APPLICANT: Makino, Yuji
; APPLICANT: Suzuki, Yoshiki
; TITLE OF INVENTION: PEPTIDE PROTEINACEOUS DRUG NASAL
; TITLE OF INVENTION: POWDER COMPOSITION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/407,000
; FILING DATE: 29-MAR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/JP94/01257
; FILING DATE: 29-JUL-1994
; APPLICATION NUMBER: JP-A-5-206922
; FILING DATE: 30-JUL-1993
; APPLICATION NUMBER: JP-A-5-235841
; FILING DATE: 30-AUG-1993
; APPLICATION NUMBER: JP-A-6-1644
; FILING DATE: 12-JAN-1994

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-407-000-6

Query Match 100.0%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
|||
Db 1 AAPF 4

RESULT 7
US-07-890-422B-28
; Sequence 28, Application US/07890422B
; Patent No. 5602102
; GENERAL INFORMATION:
; APPLICANT: THIELE, DWAIN L.
; APPLICANT: LIPSKY, PETER E.
; APPLICANT: MCGUIRE, MICHAEL J.
; TITLE OF INVENTION: DIPEPTIDYL PEPTIDASE-I
; TITLE OF INVENTION: INHIBITORS AND USES THEREOF
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/890,422B
; FILING DATE: 19920529
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MAYFIELD, DENISE L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: UTSD:296/MAY
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-320-7200
; TELEFAX: 512-474-7577
; TELEX: NOT APPLICABLE
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acid residues
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-890-422B-28

Query Match 100.0%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
|||
Db 1 AAPF 4

RESULT 8

US-08-276-936A-2
; Sequence 2, Application US/08276936A
; Patent No. 5612194
; GENERAL INFORMATION:
; APPLICANT: Harvey Rubin, Barry Cooperman, No. 5612194man Schecter,
; APPLICANT: Michael Plotkin, Zhi Wang
; TITLE OF INVENTION: Methods of Producing Effective
; TITLE OF INVENTION: Recombinant Serine Protease Inhibitors and Uses of
These
; TITLE OF INVENTION: Inhibitors
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,936A
; FILING DATE: July 19, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 221,078
; FILING DATE: March 31, 1994
; APPLICATION NUMBER: 221,171
; FILING DATE: March 31, 1994
; APPLICATION NUMBER: 005,908
; FILING DATE: January 15, 1993
; APPLICATION NUMBER: 735,335
; FILING DATE: July 24, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: PENN-0027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-276-936A-2

Query Match 100.0%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
|||
Db 1 AAPF 4

RESULT 9

US-08-345-820B-2

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; Sequence 2, Application US/08345820B
; Patent No. 5618792
; GENERAL INFORMATION:
;   APPLICANT:
;   TITLE OF INVENTION:  SUBSTITUTED HETEROCYCLIC COMPOUNDS USEFUL AS
;   TITLE OF INVENTION:  INHIBITORS OF (SERINE PROTEASES) HUMAN NEUTROPHIL
ELASTASE
;   NUMBER OF SEQUENCES:  4
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/345,820B
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  4 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-345-820B-2
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Query Match          100.0%;  Score 4;  DB 1;  Length 4;
Best Local Similarity 100.0%;  Pred. No. 2.5e+05;
Matches      4;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;
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Qy      1 AAPF 4
        ||||
Db      1 AAPF 4
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RESULT 10

US-08-544-143A-3

```
; Sequence 3, Application US/08544143A
; Patent No. 5646028
; GENERAL INFORMATION:
;   APPLICANT:  Leigh, Scott D.
;   TITLE OF INVENTION:  NOVEL ALKALINE PROTEASE AND USES
;   TITLE OF INVENTION:  THEREOF
;   NUMBER OF SEQUENCES:  22
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Majestic, Parsons, Siebert & Hsue
;     STREET:  Four Embarcadero Center, Suite 1100
;     CITY:  San Francisco
;     STATE:  California
;     COUNTRY:  U.S.A.
;     ZIP:  94111-4121
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/544,143A
; FILING DATE: 17-OCT-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: de Runtz, K. Alison
; REGISTRATION NUMBER: 37,119
; REFERENCE/DOCKET NUMBER: 0409.054US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-362-5556
; TELEFAX: 415-362-5418
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-544-143A-3

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Query Match          100.0%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 AAPF 4
        ||||
Db      1 AAPF 4

```

RESULT 11

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US-08-397-602A-9
; Sequence 9, Application US/08397602A
; Patent No. 5646044
; GENERAL INFORMATION:
; APPLICANT: Wilson, Charles R
; APPLICANT: Tang, Maria R
; APPLICANT: Berger, Harald
; APPLICANT: Christianson, Teresa M
; APPLICANT: Hansen, Dieter
; TITLE OF INVENTION: Expression Systems for the Production
; TITLE OF INVENTION: of Target Proteins in Bacillus
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henkel Corporation Law Department
; STREET: 140 Germantown Pike, Suite 150
; CITY: Plymouth Meeting
; STATE: PA
; COUNTRY: USA
; ZIP: 19462
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,602A

```

```

; FILING DATE: 02-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jaeschke, Wayne C
; REGISTRATION NUMBER: 21,062
; REFERENCE/DOCKET NUMBER: D8969/M4828
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 832-2200
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "N-SUCCINYL"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note=
; OTHER INFORMATION: "P-NITROANILIDE"
US-08-397-602A-9

```

```

Query Match          100.0%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

QY      1 AAPF 4
        ||||
Db      1 AAPF 4

```

RESULT 12

US-08-437-029-5

```

; Sequence 5, Application US/08437029
; Patent No. 5668107
; GENERAL INFORMATION:
; APPLICANT: Miller, Edward J.
; TITLE OF INVENTION: Compositions and Methods for
; TITLE OF INVENTION: Inhibiting Elastase
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/08/437,029
; FILING DATE: 08 May 95
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 017066-000620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-437-029-5

Query Match 100.0%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPF 4
|||
Db 1 AAPF 4

RESULT 13

US-08-424-022-19

; Sequence 19, Application US/08424022
; Patent No. 5677146
; GENERAL INFORMATION:
; APPLICANT: Foster, Donald C
; APPLICANT: Sprecher, Cindy
; APPLICANT: No. 5677146ris, Kjeld
; TITLE OF INVENTION: NOVEL HUMAN AMYLOID PROTEIN PRECURSOR
; TITLE OF INVENTION: HOMOLOG AND KUNITZ-TYPE INHIBITOR
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 4225 Roosevelt Way, N.E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,022
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/985,692

```

; FILING DATE: 02-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31-684
; REFERENCE/DOCKET NUMBER: 92-21C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-547-8080 ext 322
; TELEFAX: 206-548-2329
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..4
; OTHER INFORMATION: /label= ALA-1
; OTHER INFORMATION: /note= "Amino terminal alanine residue is capped
; OTHER INFORMATION: with a succinyl group"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..4
; OTHER INFORMATION: /label= Phe-4
; OTHER INFORMATION: /note= "Carboxyl-terminal phenylalanine residue is
; OTHER INFORMATION: capped with p-nitroanil..."
US-08-424-022-19

```

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Query Match          100.0%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

QY      1 AAPF 4
        ||||
Db      1 AAPF 4

```

RESULT 14

```

US-08-439-534-10
; Sequence 10, Application US/08439534
; Patent No. 5719041
; GENERAL INFORMATION:
; APPLICANT: Lazarus, Robert A.
; APPLICANT: Dennis, Mark S.
; APPLICANT: Ulmer, Jana S.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING
; TITLE OF INVENTION: ECOTIN AND HOMOLOGS THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,534
; FILING DATE: 11-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/319501
; FILING DATE: 04-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/121004
; FILING DATE: 14-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0859C1D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-439-534-10

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Query Match          100.0%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 AAPF 4
        ||||
Db      1 AAPF 4

```

RESULT 15

US-08-434-959-3

```

; Sequence 3, Application US/08434959
; Patent No. 5736520
; GENERAL INFORMATION:
; APPLICANT: Bey, Philippe
; APPLICANT: Angelastro, Michael R
; APPLICANT: Mehdi, Shujaath
; TITLE OF INVENTION: No. 5736520el Peptidase Inhibitors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marion Merrell Dow Inc.
; STREET: 2110 East Galbraith Rd.
; CITY: Cincinnati P. O. Box 156300
; STATE: Ohio
; COUNTRY: USA
; ZIP: 45215-6300
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/434,959
;      FILING DATE:
;      CLASSIFICATION:  514
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/750,439
;      FILING DATE:  20-AUG-1991
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/454,803
;      FILING DATE:  21-DEC-1989
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/439,201
;      FILING DATE:  20-NOV-1989
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/416,817
;      FILING DATE:  04-OCT-1989
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/254,762
;      FILING DATE:  07-OCT-1988
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Nesbitt, Stephen L
;      REGISTRATION NUMBER:  28,981
;      REFERENCE/DOCKET NUMBER:  M01368F US
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (513) 948-7965
;      TELEFAX:  (513) 948-7961
;      TELEX:  214320
;      INFORMATION FOR SEQ ID NO:  3:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  peptide
US-08-434-959-3

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Query Match          100.0%;  Score 4;  DB 1;  Length 4;
Best Local Similarity 100.0%;  Pred. No. 2.5e+05;
Matches      4;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

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Qy          1 AAPF 4
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Db          1 AAPF 4

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Job time : 11.5714 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 12:16:11 ; Search time 28.5714 Seconds
(without alignments)
22.222 Million cell updates/sec

Title: US-10-033-526-1
Perfect score: 4
Sequence: 1 AAPF 4

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 50015

Minimum DB seq length: 4

Maximum DB seq length: 6

Post-processing: Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

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- 2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
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- 9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
- 10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
- 11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
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- 13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
- 14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
- 15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
- 16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
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- 22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
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- 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	4	100.0	4	5	AAP40459	N-terminal polyhyd	
2	4	100.0	4	11	AAR04012	Peptidase substrat	
3	4	100.0	4	12	AAR10887	Peptide component	
4	4	100.0	4	12	AAR11223	Ketone analogue pr	
5	4	100.0	4	13	AAR29964	Cathepsin G inhibi	
6	4	100.0	4	14	AAR34258	Chromogenic peptid	
7	4	100.0	4	14	AAR38410	Cathepsin G inhibi	
8	4	100.0	4	14	AAR44109	Aminonaphthalene p	
9	4	100.0	4	15	AAR52024	Bacillus alkali pr	
10	4	100.0	4	15	AAR46223	Serine protease in	
11	4	100.0	4	15	AAR53781	Sequence of intern	
12	4	100.0	4	16	AAR72920	Substrate for pept	
13	4	100.0	4	16	AAR72876	Substrate for pept	
14	4	100.0	4	16	AAR77315	Porphyromonas ging	
15	4	100.0	4	16	AAR77196	Cell proliferation	
16	4	100.0	4	17	AAR85709	Degradable peptide	
17	4	100.0	4	18	AAW52606	Serine protease-in	
18	4	100.0	4	18	AAW30747	Substrate peptide	
19	4	100.0	4	18	AAW24567	Substrate for seri	
20	4	100.0	4	18	AAW08165	Proteinase site of	
21	4	100.0	4	18	AAW12810	Synthetic substrat	
22	4	100.0	4	19	AAW79700	B. subtilis subtil	
23	4	100.0	4	19	AAW76694	B. subtilis subtil	
24	4	100.0	4	19	AAW61357	Synthetic oligopep	
25	4	100.0	4	19	AAW51451	Indicator for dete	
26	4	100.0	4	19	AAW51610	Peptide conjugated	
27	4	100.0	4	20	AAM48424	Alkaline protease-	
28	4	100.0	4	20	ABB07072	Alkaline protease	
29	4	100.0	4	20	AAW84189	Peptide comprising	
30	4	100.0	4	21	AAB20774	Chymotrypsin enzym	
31	4	100.0	4	21	AAB03092	Substrate peptide	
32	4	100.0	4	21	AAB01922	Synthetic PPIase s	
33	4	100.0	4	21	AAV91025	Model substrate pe	
34	4	100.0	4	21	AAV97813	Protease peptide s	
35	4	100.0	4	21	AAV80465	Chymase inhibitor	
36	4	100.0	4	21	AAV76808	Chymotrypsin subst	
37	4	100.0	4	21	AAV78789	Subtilisin substra	
38	4	100.0	4	21	AAV49452	Cathepsin G peptid	
39	4	100.0	4	21	AAV59632	Peptidylprolyl cis	
40	4	100.0	4	22	AAU07699	Ztryp3 substrate u	
41	4	100.0	4	22	AAB82792	Peptide substrate	
42	4	100.0	4	22	AAG64601	Model peptide subs	
43	4	100.0	4	22	AAG64496	Artificial substra	
44	4	100.0	4	22	AAE04342	Human peptide #2,	
45	4	100.0	4	22	AAB98623	Peptide #2. Unide	

ALIGNMENTS

RESULT 1

AAP40459

ID AAP40459 standard; Protein; 4 AA.

XX

AC AAP40459;

XX

DT 25-MAR-2003 (updated)

DT 09-JAN-2003 (updated)

DT 27-NOV-1991 (first entry)

XX

DE N-terminal polyhydroxyalkanoyl peptide.

XX

KW Polyhydroxyalkanoyl peptide; protease; peptidase; prodrug.

XX

OS Unidentified.

XX

PN EP126685-A.

XX

PD 28-NOV-1984.

XX

PF 15-MAY-1984; 84EP-0400984.

XX

PR 16-MAY-1983; 83FR-0008051.

XX

PA (CNRS) CENT NAT RECH SCI.

XX

PI Monsigny M, Mayer R;

XX

DR WPI; 1984-296065/48.

XX

PT N-terminal polyhydroxyalkanoyl peptide and aminoacid derivs. - opt.

PT having C-terminal active gps., e.g. chloroquine, are water-soluble

PT antitumour or antiparasitic cpds. and protease targets.

XX

PS Claim 11; page 15; 20pp; french.

XX

CC The peptide is polyhydroxyalkanoyl-L-Ala-L-Ala-L-Pro-L-Phe-X. X is
 CC R2-NH- derived from an aromatic amine, eg P-nitro-aniline, alpha-
 CC or beta-naphthylamine, or it is R3NH derived from an amino drug, eg
 CC daunorubicin or chloroquine, or it is a gp. which may confer
 CC activity, eh H, OH, CH2Cl. When X is the residue of a drug, the
 CC cpd. is a prodrug in which the peptide is the substrate for a
 CC specific protease secreted by the target cell for the active drug,
 CC eg tumour cells or microorganism pathogens, eg Plasmodium
 CC falciparum. Due to the polyhydroxy gp., the cpds. are very soluble
 CC in water or buffer soln. and are able to be used at high concn. The
 CC cpds. also allow the detection of proteases and peptidases and
 CC allow easy determination of the best substrate for a particular
 CC protease.

CC (Updated on 09-JAN-2003 to add missing OS field.)

CC (Updated on 25-MAR-2003 to correct PD field.)

CC (Updated on 25-MAR-2003 to correct PR field.)

CC (Updated on 25-MAR-2003 to correct PA field.)

XX

SQ Sequence 4 AA;

Query Match

100.0%; Score 4; DB 5; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
|||
Db 1 AAPF 4

RESULT 2

AAR04012

ID AAR04012 standard; peptide; 4 AA.

XX

AC AAR04012;

XX

DT 25-MAR-2003 (updated)

DT 19-NOV-1991 (first entry)

XX

DE Peptidase substrate analogues having peptidase inhibition activity.

XX

KW Elastase; plasminogen activator; cathepsin; calpain; enkephalinase;

KW Angiotensin converting enzyme.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 4

FT /label= Terminal modified from -COOH to -COCOR

FT /note= "R = alkyl group or -H"

XX

PN EP363284-A.

XX

PD 11-APR-1990.

XX

PF 06-OCT-1989; 89EP-0402762.

XX

PR 07-OCT-1988; 88US-0254762.

PR 06-OCT-1989; 89EP-0402763.

XX

PA (RICH) MERRELL DOW PHARM INC.

PA (RICH) MERRELL PHARM INC.

XX

PI Bey P, Angelastro M, Mehdi S;

XX

DR WPI; 1990-109579/15.

XX

PT New peptidase substrate analogue cpds. - useful as protease

PT inhibitors in treatment of disease states.

XX

PS Claim 5; Page 26; 33pp; English.

XX

CC The analogues may be useful in treatment of a variety of disease
CC states. The scissile amide group is replaced with H or a substituted
CC Carbon moiety effectively inhibiting the activity of peptidases such
CC as elastase, plasmin thrombin, urokinase etc.
CC (Updated on 25-MAR-2003 to correct PA field.)

XX

SQ Sequence 4 AA;

Query Match 100.0%; Score 4; DB 11; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
 ||||
Db 1 AAPF 4

RESULT 3

AAR10887

ID AAR10887 standard; Protein; 4 AA.

XX

AC AAR10887;

XX

DT 10-APR-1991 (first entry)

XX

DE Peptide component of pentafluoroethylcarbonyl analogue.

XX

KW Protease inhibitor; rheumatoid arthritis; thrombosis; psoriasis;
KW male contraceptive.

XX

OS Synthetic.

XX

PN EP410411-A.

XX

PD 30-JAN-1991.

XX

PF 25-JUL-1990; 90EP-0114250.

XX

PR 26-JUL-1989; 89US-0385624.

XX

PA (RICH) MERRELL DOW PHARM INC.

XX

PI Bey P, Peet NP, Angelastro MR, Mehdi S;

XX

DR WPI; 1991-030811/05.

XX

PT Novel serine-, carboxylic acid-and metallo-proteinase-inhibitors

PT - inhibit range of proteinase(s) in treating rheumatoid

PT arthritis, thrombosis and psoriasis, also is a male contraceptive

XX

PS Claim 5; page 25; 40pp; English.

XX

CC This peptide is the R1 gp. of the cpd. of formula: R1NHCH(R2)-
CC COCF2CF3. This cpd. is a peptidase substrate analogue and is a
CC specific enzyme inhibitor for a range of proteases, e.g. serine-,
CC carboxylic acid-, and metallo-proteases. It is useful in the
CC treatment of rheumatoid arthritis, thrombosis and psoriasis and is
CC also used as a male contraceptive. See also AAR10876-83, AAR10886 and
CC AAR10888.

XX

SQ Sequence 4 AA;

Query Match 100.0%; Score 4; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
 ||||
Db 1 AAPF 4

RESULT 4

AAR11223

ID AAR11223 standard; Protein; 4 AA.

XX

AC AAR11223;

XX

DT 24-MAY-1991 (first entry)

XX

DE Ketone analogue protease inhibitor #2.

XX

KW protease inhibitor; antiinflammatory agent; hypotensive; analgesic;

KW antiproliferative agent; antidemyelinating agent; antithrombotic.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /label= Methoxysuccinyl-Ala

FT Modified-site 4

FT /label= Phe-carboxyoxalyl

XX

PN EP417721-A.

XX

PD 20-MAR-1991.

XX

PF 11-SEP-1990; 90EP-0117461.

XX

PR 11-SEP-1989; 89US-0405491.

XX

PA (RICH) MERRELL DOW PHARM INC.

XX

PI Flynn GA, Bey P;

XX

DR WPI; 1991-081980/12.

XX

PT New ketone analogue peptidase and isomerase inhibitors - for

PT inhibition of leukocyte elastase, cathepsin G, thrombin,

PT chymotrypsin, plasmin etc.

XX

PS Claim 5; Page 26; 50pp; English.

XX

CC This peptide is a specific example of a highly generic protease
CC inhibitor useful for medical purposes. The peptide analogues include
CC inhibitors of urokinase, renin, cathepsin D, etc. which can be used
CC as anti-proliferative agents and abortifacients, hypotensives,
CC antiinflammatory and antidemyelinating agents, respectively.
CC See also AAR11222 and AAR11224-R11238.

XX

SQ Sequence 4 AA;

Query Match 100.0%; Score 4; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPF 4
 ||||
Db 1 AAPF 4

RESULT 5

AAR29964

ID AAR29964 standard; peptide; 4 AA.

XX

AC AAR29964;

XX

DT 25-MAR-2003 (updated)

DT 19-APR-1993 (first entry)

XX

DE Cathepsin G inhibiting fragment.

XX

KW Cathepsin G; elastase; connective tissue; degradation; protease;

KW gout; rheumatoid arthritis; emphysema; ARDS;

KW adult respiratory distress syndrome; para-phenylene.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal amino acids of the peptides of
FT AAR29963-64 are pref. linked by
FT -C(O)-phenylene-C(O)-, esp. wherein the
FT phenylene is a para-phenylene gp."

FT Modified-site 4

FT /note= "C-terminal Phe is in keto form, i.e. OH
FT replaced by CGIM, pref. CF3 or CF2CF3"

XX

PN WO9220357-A1.

XX

PD 26-NOV-1992.

XX

PF 21-APR-1992; 92WO-US03288.

XX

PR 23-MAY-1991; 91US-0704499.

XX

PA (RICH) MERRELL DOW PHARM INC.

XX

PI Angelastro MR, Bey P, Doherty NS, Janusz MJ, Mehdi S;

PI Peet NP;

XX

DR WPI; 1992-415461/50.

XX

PT New peptide derivs. used as cathepsin G and elastase inhibitors -

PT for treating gout, rheumatoid arthritis, inflammatory disorders,

PT emphysema and adult respiratory distress syndrome

XX

PS Claim 13-17; Page 52; 53pp; English.

XX

CC This sequence is an example of a highly generic formula.
 CC Inhibitors of cathepsin G and elastase for preventing connective
 CC tissue degradation are chemically linked inhibitors of the proteases
 CC elastase (pref. the peptide of AAR29963, or Lys(2CBz)-Pro-Val or
 CC Val-Pro-Val) and cathepsin G (pref. the peptide of AAR29964, or
 CC Val-Pro-Phe or Phe).
 CC The N-terminal amino acids of the peptides of AAR29963-64 are pref.
 CC linked by -C(O)-phenylene-C(O)-, esp. wherein the phenylene is a
 CC para-phenylene gp.
 CC The cpds. have an anti-inflammatory effect useful in the treatment
 CC of gout, rheumatoid arthritis and other inflammatory diseases and
 CC to prevent elastin mediated tissue damage. They can also be used
 CC in the treatment of emphysema and adult respiratory distress syndrome.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 4 AA;

Query Match 100.0%; Score 4; DB 13; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPF 4
 ||||
 Db 1 AAPF 4

RESULT 6

AAR34258

ID AAR34258 standard; peptide; 4 AA.

XX

AC AAR34258;

XX

DT 25-MAR-2003 (updated)

DT 19-AUG-1993 (first entry)

XX

DE Chromogenic peptide substrate for peptidase assay.

XX

KW Alkaline protease; detergent; stability.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-succinyl alanine"

FT Modified-site 4

FT /note= "Phe-p-nitroanilide"

XX

PN W09307276-A1.

XX

PD 15-APR-1993.

XX

PF 07-OCT-1992; 92WO-US08341.

XX

PR 08-OCT-1991; 91US-0772087.

XX

PA (CHEM-) CHEMGEN CORP.

PA (VIST-) VISTA CHEMICAL CO.
 XX
 PI Fodge DW, Hsiao H, Lalonde JJ;
 XX
 DR WPI; 1993-134465/16.
 XX
 PT Alkaline protease produced by bacillus stable in alkaline
 PT conditions - used in detergents and bleaches to decompose
 PT proteinaceous stains
 XX
 PS Disclosure; Page 8; 58pp; English.
 XX
 CC The peptide is a chromogenic substrate for use in a peptidase assay
 CC to test the peptidase activity of a novel alkaline protease.
 CC Detergent was found to interfere with the assay by reducing the
 CC protease activity. See also AAR34259-61 and AAR34463-66.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 4 AA;

Query Match 100.0%; Score 4; DB 14; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
 ||||
 Db 1 AAPF 4

RESULT 7

AAR38410

ID AAR38410 standard; Protein; 4 AA.

XX

AC AAR38410;

XX

DT 29-OCT-1993 (first entry)

XX

DE Cathepsin G inhibitor peptide #1.

XX

KW Inflammatory disease; prevention; rheumatoid arthritis; emphysema;

KW neutrophil-mediated connective tissue degradation; gout; elastase;

KW inhibition; adult respiratory distress syndrome.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Linked via a linking chain such as

FT -CO-phenylene-CO- to the N-terminal of a

FT Cathepsin G inhibiting molecule as described

FT in AAR38410-11"

FT Modified-site 4

FT /note= "May opt. be modified by COCOR, CF2CF3, CF3,

FT CHF2, COOR3, CONHR3, CF2CHR3CONHR, H, alkyl,

FT aryl, aralkyl or COR; where R3 is H, alkyl,

FT phenyl or benzyl and R is OH or alkoxy"

XX

PN ZA9203602-A.
 XX
 PD 24-FEB-1993.
 XX
 PF 18-MAY-1992; 92ZA-0003602.
 XX
 PR 23-MAY-1991; 91US-0704499.
 XX
 PA (RICH) MERRELL DOW PHARM INC.
 XX
 PI Angelastro MM, Bey P, Doherty NS, Janusz MJ, Mehdi S;
 PI Peet NP;
 XX
 DR WPI; 1993-197380/24.
 XX
 PT New cathepsin G and elastase inhibitors - prevents connective
 PT tissue degradation
 XX
 PS Claim 13-17; Page 52; 55pp; English.
 XX
 CC The sequences given in AAR38410-11 are cathepsin G inhibiting peptides
 CC which were produced by standard peptide synthesis methods. In the
 CC context of the invention one of these peptides may be linked via
 CC their N-termini to an elastase inhibiting peptide (see features
 CC table). The peptide conjugates may be used to prevent neutrophil-
 CC mediated connective tissue degradation associated with inflammatory
 CC diseases eg. gout and rheumatoid arthritis. They may also be used
 CC for preventing elastin-mediated tissue damage in the treatment of
 CC emphysema and adult respiratory distress syndrome.
 XX
 SQ Sequence 4 AA;

Query Match 100.0%; Score 4; DB 14; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
 ||||
 Db 1 AAPF 4

RESULT 8

AAR44109

ID AAR44109 standard; peptide; 4 AA.
 XX
 AC AAR44109;
 XX
 DT 25-MAR-2003 (updated)
 DT 16-MAY-1994 (first entry)
 XX
 DE Aminonaphthalene propyl sulphamide tetrapeptide.
 XX
 KW chymotrypsin assay; ansa-substrate; detector group.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers

FT Modified-site 1
 FT /label= OTHER
 FT /note= "Suc-Ala (Claim 1) or Z-Ala (Claim 2)"
 FT Modified-site 4
 FT /label= OTHER
 FT /note= "Phe-NH- (1,5-naphthylene) -SO₂NH-C₃H₇"
 XX
 PN SU1771478-A3.
 XX
 PD 23-OCT-1992.
 XX
 PF 20-JUL-1990; 90SU-4872552.
 XX
 PR 20-JUL-1990; 90SU-4872552.
 XX
 PA (ALIB=) AS LITH BIOCHEM INST.
 PA (ASMO=) AS USSR MOLECULAR GENETICS.
 XX
 PI Nedospasov AA, Palaima AI, Yanchene RA;
 XX
 DR WPI; 1993-358242/45.
 XX
 PT Prepn. of new succinyl-alanyl-alanyl-propyl-phenylalanyl-amino-
 PT naphthalen-propyl-sulphamide - for use as ansa-substrate in the
 PT quantitative determin. of chymotrypsin
 XX
 PS Claim 1 and 2; Column 8; 4pp; Russian.
 XX
 CC 5-(N-succinyl-alanyl-alanyl-prolyl-phenylalanyl)aminonaphthalene-1-
 CC (N-propyl)sulphamide (Claim 1) and 5-(N-benzyloxycarbonyl-alanyl-
 CC alanyl-prolyl-phenylalanyl)aminonaphthalene-1-(N-propyl)sulphamide
 CC (Claim 2) are prepared by initially reacting N-benzyloxycarbonyl-
 CC phenylalanine with isobutyl chloroformate in tetrahydrofuran
 CC followed by reaction with 5-aminonaphthalene-1-(N-propyl)sulphamide.
 CC The new compounds are used as detector groups in quantitative
 CC determination of chymotrypsin.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 4 AA;

 Query Match 100.0%; Score 4; DB 14; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
 ||||
 Db 1 AAPF 4

RESULT 9
 AAR52024
 ID AAR52024 standard; peptide; 4 AA.
 XX
 AC AAR52024;
 XX
 DT 28-NOV-1994 (first entry)
 XX

DE Bacillus alkali protease substrate.
 XX
 KW Bacillus NKS-21 alkali protease; hydrolysis; thermostable enzyme;
 KW detergent stable.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /label= OTHER
 FT /note= "Suc-Ala"
 FT Modified-site 4
 FT /label= OTHER
 FT /note= "Phe-MCA"
 XX
 PN JP06070765-A.
 XX
 PD 15-MAR-1994.
 XX
 PF 08-OCT-1992; 92JP-0296360.
 XX
 PR 10-JUL-1992; 92JP-0207302.
 XX
 PA (SHOW) SHOWA DENKO KK.
 XX
 DR WPI; 1994-128672/16.
 XX
 PT New alkali protease stable to heat and detergent - useful as
 PT industrial enzyme, eg in washing compositions
 XX
 PS Claim 1; Page 2; 10pp; Japanese.
 XX
 CC A novel alkali protease obtained from Bacillus NKS-21 is defined by
 CC its physico-chemical properties including substrate specificity for
 CC the tetrapeptide AAR52024.
 XX
 SQ Sequence 4 AA;

 Query Match 100.0%; Score 4; DB 15; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
 ||||
 Db 1 AAPF 4

RESULT 10
 AAR46223
 ID AAR46223 standard; peptide; 4 AA.
 XX
 AC AAR46223;
 XX
 DT 04-AUG-1994 (first entry)
 XX
 DE Serine protease inhibitor tetrapeptide.
 XX

KW Prevention; schistosomiasis; parasite; infection; prevention;
KW parasitic penetration; skin; cercariae; anti-penetrant.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "BG(peptide blocking gp.) attached".

FT Modified-site 4

FT /note= "PI(protease inhibitor), other than
FT chloromethyl ketone, attached"

XX

PN US5284829-A.

XX

PD 08-FEB-1994.

XX

PF 26-NOV-1991; 91US-0798565.

XX

PR 26-NOV-1991; 91US-0798565.

XX

PA (REGC) UNIV CALIFORNIA.

XX

PI Cohen FE, McKerrow JH;

XX

DR WPI; 1994-056364/07.

XX

PT Synthetic tetra:peptide(s) with an N-terminal blocking gp. and

PT C-terminal enzyme inhibitor - can be formulated into soaps and

PT sprays and used to prevent schistosomal skin penetration

XX

PS Disclosure; Page 7; 35pp; English.

XX

CC The sequence is that of a synthetic tetrapeptide serine protease

CC inhibitor which can be used to prevent schistosome parasite

CC infection. It may be used in a formulation as a soap, lotion,

CC cream, spray, etc. to stop parasitic penetration of the skin.

XX

SQ Sequence 4 AA;

Query Match 100.0%; Score 4; DB 15; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4

||||

Db 1 AAPF 4

RESULT 11

AAR53781

ID AAR53781 standard; Peptide; 4 AA.

XX

AC AAR53781;

XX

DT 25-MAR-2003 (updated)

DT 29-DEC-1994 (first entry)

XX

DE Sequence of internal fragment of a chromogenic substrate for
 DE cathepsin G.
 XX
 KW Enzyme; cathepsin G; protease; chromogenic substrate.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /label= Suc-Ala
 FT /note= "Succinyl group"
 FT Modified-site 4
 FT /label= Phe-pNA
 FT /note= "p-nitroanil"
 XX
 PN WO9412637-A2.
 XX
 PD 09-JUN-1994.
 XX
 PF 01-DEC-1993; 93WO-US11696.
 XX
 PR 02-DEC-1992; 92US-0985692.
 PR 19-NOV-1993; 93US-0155331.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Foster DC, Norris K, Sprecher CA;
 XX
 DR WPI; 1994-200265/24.
 XX
 PT New human Kunitz type protease inhibitor and related DNA - for
 PT treating pancreatitis and other disorders involving serine
 PT protease, also new amyloid protein precursor homologues including
 PT the inhibitor in its sequence
 XX
 PS Example; Page 63; 70pp; English.
 XX
 CC Protease inhibitory profiles of the Kunitz inhibitors
 CC were determined for a variety of proteases using
 CC a variety of chromogenic substrates and compared to the inhibitory
 CC activity shown by the Kunitz-type inhibitor domain of the amyloid
 CC protein precursor and bovine aprotinin. The substrate AAR53780
 CC was tested using the protease leukocyte elastase.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 4 AA;

Query Match 100.0%; Score 4; DB 15; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
 ||||
 Db 1 AAPF 4

RESULT 12

AAR72920

ID AAR72920 standard; Peptide; 4 AA.

XX

AC AAR72920;

XX

DT 25-MAR-2003 (updated)

DT 29-NOV-1995 (first entry)

XX

DE Substrate for peptidyl prolyl cis trans isomerase alpha.

XX

KW Escherichia coli; protein conformation; folding; acceleration;

KW PPIase-alpha; peptidyl prolyl cis trans isomerase alpha;

KW catalysis; isomerisation; prolyl peptide bond.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-succinyl-Ala"

FT Modified-site 4

FT /note= "Phe-MCA (sic)"

XX

PN EP647714-A1.

XX

PD 12-APR-1995.

XX

PF 19-JUL-1990; 94EP-0203612.

XX

PR 19-JUL-1989; 89JP-0184738.

PR 06-OCT-1989; 89JP-0260244.

PR 29-DEC-1989; 89JP-0344705.

PR 19-JUL-1990; 90EP-0307914.

XX

PA (TOFU) TONEN CORP.

XX

PI Hayano T, Katou S, Maki N, Suzuki M, Takahashi N;

XX

DR WPI; 1995-140756/19.

XX

PT New E.coli peptidyl prolyl cis trans isomerase beta - used to

PT accelerate the folding of proteins, partic. for activation of

PT inactive recombinant proteins

XX

PS Disclosure; Page 5; 85pp; English.

XX

CC To measure the activity of E. coli PPIase-alpha (peptidyl prolyl cis

CC trans isomerase alpha), the PPIase and CsA (cyclosporine A) are

CC added in the cell and mixed for 1 minute. Then, this peptide is

CC added and incubated, and chymotrypsin added to start the reaction.

CC The effect of CsA on the inhibition of the PPIase activity can be

CC detected by varying the amt. of the CsA added. The inventors are

CC claiming a PPIase-beta.

CC (Updated on 25-MAR-2003 to correct PN field.)

CC (Updated on 25-MAR-2003 to correct PF field.)

CC (Updated on 25-MAR-2003 to correct PR field.)

XX

SQ Sequence 4 AA;

Query Match 100.0%; Score 4; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
|||
Db 1 AAPF 4

RESULT 13

AAR72876

ID AAR72876 standard; Peptide; 4 AA.

XX

AC AAR72876;

XX

DT 25-MAR-2003 (updated)

DT 29-NOV-1995 (first entry)

XX

DE Substrate for peptidyl prolyl cis trans isomerase alpha.

XX

KW Escherichia coli; protein conformation; folding; acceleration;

KW PPIase-alpha; peptidyl prolyl cis trans isomerase alpha;

KW catalysis; isomerisation; prolyl peptide bond.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-succinyl-Ala"

FT Modified-site 4

FT /note= "Phe-MCA (sic)"

XX

PN EP647713-A1.

XX

PD 12-APR-1995.

XX

PF 19-JUL-1990; 94EP-0203610.

XX

PR 19-JUL-1989; 89JP-0184738.

PR 06-OCT-1989; 89JP-0260244.

PR 29-DEC-1989; 89JP-0344705.

PR 19-JUL-1990; 90EP-0307914.

XX

PA (TOFU) TONEN CORP.

XX

PI Hayano T, Katou S, Maki N, Suzuki M, Takahashi N;

XX

DR WPI; 1995-140755/19.

XX

PT New E.coli peptidyl prolyl cis trans isomerase alpha - used to

PT accelerate the folding of proteins, partic. for activation of

PT inactive recombinant proteins

XX

PS Disclosure; Page 5; 85pp; English.

XX

CC To measure the activity of E. coli PPIase-alpha (peptidyl prolyl cis
 CC trans isomerase alpha), the PPIase and CsA (cyclosporine A) are
 CC added in the cell and mixed for 1 minute. Then, this peptide is
 CC added and incubated, and chymotrypsin added to start the reaction.
 CC The effect of CsA on the inhibition of the PPIase activity can be
 CC detected by varying the amt. of the CsA added. The inventors are
 CC claiming the PPIase-alpha.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 4 AA;

Query Match 100.0%; Score 4; DB 16; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
 ||||
 Db 1 AAPF 4

RESULT 14

AAR77315

ID AAR77315 standard; Protein; 4 AA.

XX

AC AAR77315;

XX

DT 28-FEB-1996 (first entry)

XX

DE Porphyromonas gingivalis protease substrate.

XX

KW Protease; periodontal disease; pathogenic microbe; diagnosis;
 KW substrate.

XX

OS Synthetic.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Modified-site	1
----	---------------	---

FT		/note= "Suc-Ala"
----	--	------------------

FT	Modified-site	4
----	---------------	---

FT		/note= "MCA-Phe"
----	--	------------------

XX

PN JP07135973-A.

XX

PD 30-MAY-1995.

XX

PF 15-NOV-1993; 93JP-0307084.

XX

PR 15-NOV-1993; 93JP-0307084.

XX

PA (SUNR) SUNTORY LTD.

XX

DR WPI; 1995-227397/30.

XX

PT An enzyme originated from a periodontal disease pathogenic microbe -
 PT and an antibody against the enzyme, for the determination of the

PT progress and activity of the disease

XX

PS Example; Page 7; 15pp; Japanese.

XX

CC AAR77315 is a target substrate for a Porphyromonas gingivalis (a
CC periodontal disease pathogenic microbe) protease. An antibody
CC raised against the enzyme can be used to diagnose the presence
CC and progress of a periodontal disease, caused by a pathogenic
CC microbe.

XX

SQ Sequence 4 AA;

Query Match 100.0%; Score 4; DB 16; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPF 4

||||

Db 1 AAPF 4

RESULT 15

AAR77196

ID AAR77196 standard; peptide; 4 AA.

XX

AC AAR77196;

XX

DT 27-FEB-1996 (first entry)

XX

DE Cell proliferation enzyme proteinase activity substrate peptide #1.

XX

KW Proteinase; cell growth-stimulating protein; hydrolysis;

KW macrophage chemotactic action; serine protease inhibitor; wound;

KW gastric ulcer; leg ulcer; bed sore.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /label= Succinyl-Ala

FT Modified-site 4

FT /note= "Modified by 4-methyl-coumaryl-7-amide"

XX

PN EP661293-A2.

XX

PD 05-JUL-1995.

XX

PF 22-DEC-1994; 94EP-0120406.

XX

PR 29-DEC-1993; 93JP-0351225.

XX

PA (SANW) SANWA KAGAKU KENKYUSHO CO.

XX

PI Awaya J, Uesaka H, Watanabe K, Yamaguchi T;

XX

DR WPI; 1995-233274/31.

XX

PT Protein derived from Clostridium perfringens FERM BP-4584 -
PT stimulates cell proliferation and has macrophage chemotactic action

XX

PS Example; Page 8; 14pp; English.

XX

CC The sequences given in AAR77196-200 are peptides which were used to
CC demonstrate the proteinase activity of the cell growth-stimulating
CC protein of the invention. The protein was seen to selectively
CC hydrolyse synthetic substrates having an aromatic amino acid at the
CC C-terminal. The response to the peptide given in AAR77196 was
CC particularly high. The cell growth-stimulating protein has a mol.
CC wt. of 420 +/- 40 kD and a single subunit mol. wt. of 130 +/- 20 kD.
CC It has an isoelectric point of 4.8 and has cell growth stimulating
CC action and macrophage chemotactic action, as well as proteinase
CC activity. Its enzymatic activity decreases in the presence of a
CC serine protease inhibitor, increase in the presence of various metal
CC ions, and is stabilised in the presence of calcium ion. The protein is
CC particularly useful for the treatment of wounds, gastric and leg ulcers,
CC eg. bed sores.

XX

SQ Sequence 4 AA;

Query Match 100.0%; Score 4; DB 16; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4

||||

Db 1 AAPF 4

Search completed: December 30, 2003, 12:23:05

Job time : 29.5714 secs

OM protein - protein search, using sw model

Run on: December 30, 2003, 12:23:47 ; Search time 20.2857 Seconds
(without alignments)
39.243 Million cell updates/sec

Title: US-10-033-526-1
Perfect score: 4
Sequence: 1 AAPF 4

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 724715 seqs, 199017464 residues

Word size : 0

Total number of hits satisfying chosen parameters: 18921

Minimum DB seq length: 4

Maximum DB seq length: 6

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%				
Result		Query				
No.	Score	Match	Length	DB	ID	Description

1	4	100.0	4	9	US-09-757-908A-15	Sequence 15, Appl
2	4	100.0	4	10	US-09-117-380B-2	Sequence 2, Appli
3	4	100.0	4	10	US-09-935-744-1	Sequence 1, Appli
4	4	100.0	4	12	US-10-373-794-3	Sequence 3, Appli
5	4	100.0	4	14	US-10-090-624-33	Sequence 33, Appl
6	4	100.0	4	14	US-10-036-371-7	Sequence 7, Appli
7	4	100.0	4	14	US-10-040-655-10	Sequence 10, Appl
8	4	100.0	4	14	US-10-033-526-1	Sequence 1, Appli
9	4	100.0	4	14	US-10-041-006A-10	Sequence 10, Appl
10	4	100.0	4	15	US-10-209-812-6	Sequence 6, Appli
11	4	100.0	4	15	US-10-104-693-6	Sequence 6, Appli
12	4	100.0	4	15	US-10-229-346-35	Sequence 35, Appl
13	4	100.0	6	10	US-09-994-927-1	Sequence 1, Appli
14	4	100.0	6	14	US-10-033-526-4	Sequence 4, Appli
15	3	75.0	4	9	US-09-842-543-1	Sequence 1, Appli
16	3	75.0	4	9	US-09-757-908A-14	Sequence 14, Appl
17	3	75.0	4	10	US-09-117-380B-1	Sequence 1, Appli
18	3	75.0	4	10	US-09-935-744-2	Sequence 2, Appli
19	3	75.0	4	11	US-09-928-117-1	Sequence 1, Appli
20	3	75.0	4	11	US-09-876-904A-19	Sequence 19, Appl
21	3	75.0	4	12	US-10-373-794-2	Sequence 2, Appli
22	3	75.0	4	12	US-10-354-706-1	Sequence 1, Appli
23	3	75.0	4	12	US-10-350-470-10	Sequence 10, Appl
24	3	75.0	4	12	US-10-125-222-1	Sequence 1, Appli
25	3	75.0	4	12	US-10-259-609-29	Sequence 29, Appl
26	3	75.0	4	12	US-10-352-786-63	Sequence 63, Appl
27	3	75.0	4	12	US-10-352-786-65	Sequence 65, Appl
28	3	75.0	4	14	US-10-040-655-11	Sequence 11, Appl
29	3	75.0	4	14	US-10-154-507-6	Sequence 6, Appli
30	3	75.0	4	14	US-10-154-507-7	Sequence 7, Appli
31	3	75.0	4	14	US-10-154-507-13	Sequence 13, Appl
32	3	75.0	4	14	US-10-154-507-14	Sequence 14, Appl
33	3	75.0	4	14	US-10-154-507-15	Sequence 15, Appl
34	3	75.0	4	14	US-10-154-507-16	Sequence 16, Appl
35	3	75.0	4	14	US-10-033-526-2	Sequence 2, Appli
36	3	75.0	4	14	US-10-033-526-3	Sequence 3, Appli
37	3	75.0	4	14	US-10-041-006A-11	Sequence 11, Appl
38	3	75.0	4	15	US-10-025-514-33	Sequence 33, Appl
39	3	75.0	4	15	US-10-028-075B-72	Sequence 72, Appl
40	3	75.0	4	15	US-10-029-206A-72	Sequence 72, Appl
41	3	75.0	4	15	US-10-229-346-36	Sequence 36, Appl
42	3	75.0	5	12	US-10-293-086-143	Sequence 143, App
43	3	75.0	5	12	US-10-352-786-124	Sequence 124, App
44	3	75.0	5	12	US-10-352-786-126	Sequence 126, App
45	3	75.0	5	12	US-10-352-786-128	Sequence 128, App

ALIGNMENTS

RESULT 1
 US-09-757-908A-15
 ; Sequence 15, Application US/09757908A
 ; Patent No. US20020052468A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Conklin, Darrell

```
; TITLE OF INVENTION: Disulfide Core Polypeptides
; FILE REFERENCE: 98-13D1
; CURRENT APPLICATION NUMBER: US/09/757,908A
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 09/326,039
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: US 60/088,136
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-757-908A-15
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Query Match          100.0%; Score 4; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches      4; Conservative    0; Mismatches    0; Indels    0; Gaps    0;
```

```
Qy      1 AAPF 4
        ||||
Db      1 AAPF 4
```

RESULT 2

US-09-117-380B-2

```
; Sequence 2, Application US/09117380B
; Patent No. US20020119917A1
; GENERAL INFORMATION:
; APPLICANT: FRIDKIN, Matityahu
; APPLICANT: YAVIN, Eran J.
; TITLE OF INVENTION: ANTI-INFLAMMATORY PEPTIDES DERIVED FROM C-REACTIVE
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: FRIDKIN=1
; CURRENT APPLICATION NUMBER: US/09/117,380B
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: PCT/IL97/00032
; PRIOR FILING DATE: 1997-01-27
; PRIOR APPLICATION NUMBER: IL 116976
; PRIOR FILING DATE: 1996-01-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The N-terminal Ala residue is modified with a
; OTHER INFORMATION: succinyl group; the C-terminal Phe residue is
; OTHER INFORMATION: modified with a nitroanilide group.
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-117-380B-2
```

```
Query Match          100.0%; Score 4; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches      4; Conservative    0; Mismatches    0; Indels    0; Gaps    0;
```

Qy 1 AAPF 4
|||
Db 1 AAPF 4

RESULT 3

US-09-935-744-1

; Sequence 1, Application US/09935744
; Patent No. US20020137118A1
; GENERAL INFORMATION:
; APPLICANT: Inouye, Masayori
; APPLICANT: Shinde, Ujwal
; APPLICANT: Fu, Xuan
; TITLE OF INVENTION: Biologically Active Protein Folding Intermediates
; FILE REFERENCE: 266/223
; CURRENT APPLICATION NUMBER: US/09/935,744
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The sequence is part of a synthetic peptide that is used
as a sub
; OTHER INFORMATION: strate for determining the activation time of a stable
crosslinke
; OTHER INFORMATION: d intermediate conformer.
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(4)
; OTHER INFORMATION: Sequence is preceded by N-succinyl and followed by p-
nitroanilide
US-09-935-744-1

Query Match 100.0%; Score 4; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
|||
Db 1 AAPF 4

RESULT 4

US-10-373-794-3

; Sequence 3, Application US/10373794
; Publication No. US20030152564A1
; GENERAL INFORMATION:
; APPLICANT: FRIDKIN, Matityahu
; APPLICANT: YAVIN, Eran
; TITLE OF INVENTION: ANTI-INFLAMMATORY PEPTIDES DERIVED FROM C-REACTIVE
PROTEIN
; FILE REFERENCE: FRIDKIN=3
; CURRENT APPLICATION NUMBER: US/10/373,794
; CURRENT FILING DATE: 2003-02-27


```

; PRIOR APPLICATION NUMBER: US/09/446,868
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: PCT/IL98/00302
; PRIOR FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: IL 121191
; PRIOR FILING DATE: 1997-06-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: The N-terminal Ala residue is modified with a succinyl
moiety and
; OTHER INFORMATION: the C-terminal Phe residue is modified with a
nitroanilide moiety
; OTHER INFORMATION: y.
US-10-373-794-3

```

```

Query Match          100.0%; Score 4; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 AAPF 4
        ||||
Db      1 AAPF 4

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RESULT 5

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US-10-090-624-33
; Sequence 33, Application US/10090624
; Publication No. US20020132335A1
; GENERAL INFORMATION:
; APPLICANT: TAKAKURA, Hikaru
; APPLICANT: MORISHITA, Mio
; APPLICANT: SHIMOJO, Tomoko
; APPLICANT: ASADA, Kiyozo
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
; FILE REFERENCE: TAKAKURA=6
; CURRENT APPLICATION NUMBER: US/10/090,624
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: 09/445,472
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 151969/1997
; PRIOR FILING DATE: 1997-06-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

```

; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Residue 1 is modified by a succinyl group.
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Residue 4 is modified by a p-nitroaniline group.
US-10-090-624-33

Query Match 100.0%; Score 4; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
|||
Db 1 AAPF 4

RESULT 6

US-10-036-371-7
; Sequence 7, Application US/10036371
; Publication No. US20020141987A1
; GENERAL INFORMATION:
; APPLICANT: BJARNARSON, JON B.
; TITLE OF INVENTION: FISH SERINE PROTEINASES AND THEIR PHARMACEUTICAL AND
; TITLE OF INVENTION: COSMETIC USE
; FILE REFERENCE: 81691/284960
; CURRENT APPLICATION NUMBER: US/10/036,371
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/411,688
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 5086/99
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
US-10-036-371-7

Query Match 100.0%; Score 4; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
|||
Db 1 AAPF 4

RESULT 7

US-10-040-655-10
; Sequence 10, Application US/10040655
; Publication No. US20020146805A1
; GENERAL INFORMATION:

```
; APPLICANT: Andrade-Gordon, Patricia
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jian-shen
; TITLE OF INVENTION: DNA encoding the novel human serine
; TITLE OF INVENTION: protease T
; FILE REFERENCE: ORT-1032
; CURRENT APPLICATION NUMBER: US/10/040,655
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide substrate
US-10-040-655-10
```

```
Query Match          100.0%; Score 4; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches      4; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
```

```
Qy      1 AAPF 4
        ||||
Db      1 AAPF 4
```

```
RESULT 8
US-10-033-526-1
; Sequence 1, Application US/10033526
; Publication No. US20020147999A1
; GENERAL INFORMATION:
; APPLICANT: Robert W. Mahley
; APPLICANT: Yadong Huang
; TITLE OF INVENTION: Methods of Treating Disorders Related to
; TITLE OF INVENTION: APOE
; FILE REFERENCE: UCAL217
; CURRENT APPLICATION NUMBER: US/10/033,526
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 60/245,737
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-033-526-1
```

```
Query Match          100.0%; Score 4; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches      4; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
```

```
Qy      1 AAPF 4
        ||||
```

Db 1 AAPF 4

RESULT 9

US-10-041-006A-10

; Sequence 10, Application US/10041006A
; Publication No. US20020168754A1
; GENERAL INFORMATION:
; APPLICANT: Andrade-Gordon, Patricia
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jian-shen
; TITLE OF INVENTION: DNA encoding the novel human serine
; TITLE OF INVENTION: protease T
; FILE REFERENCE: ORT-1032
; CURRENT APPLICATION NUMBER: US/10/041,006A
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide substrate
US-10-041-006A-10

Query Match 100.0%; Score 4; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
|||
Db 1 AAPF 4

RESULT 10

US-10-209-812-6

; Sequence 6, Application US/10209812
; Publication No. US20030087785A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, Arne Agerlin
; APPLICANT: Osten, Claus von der
; APPLICANT: Andersen, Kim Vilbour
; APPLICANT: Ernst, Steffen
; APPLICANT: Roggen, Erwin Ludo
; TITLE OF INVENTION: A Modified Polypeptide
; FILE REFERENCE: 5666.200-US
; CURRENT APPLICATION NUMBER: US/10/209,812
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US/09/417,359
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: PA 1998 01301
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PA 1999 01418
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: 60/105,624
; PRIOR FILING DATE: 1998-10-26

; PRIOR APPLICATION NUMBER: 60/157,426
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-209-812-6

Query Match 100.0%; Score 4; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
 ||||
Db 1 AAPF 4

RESULT 11

US-10-104-693-6
; Sequence 6, Application US/10104693
; Publication No. US20030118605A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; APPLICANT: Ganshaw, Grant C.
; APPLICANT: Harding, Fiona A.
; APPLICANT: Larenas, Edmund A.
; APPLICANT: Poulouse, Ayrookaran J.
; APPLICANT: Sikorski, Elizabeth E.
; APPLICANT: Russell, Elliott P.
; TITLE OF INVENTION: Proteins Producing an Altered Immunogenic
; TITLE OF INVENTION: Response and Methods of Making and Using the Same
; FILE REFERENCE: GC683-2
; CURRENT APPLICATION NUMBER: US/10/104,693
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: succinyl-AAPF-para nitroanilide citation assay
US-10-104-693-6

Query Match 100.0%; Score 4; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
 ||||
Db 1 AAPF 4

RESULT 12

US-10-229-346-35

```

; Sequence 35, Application US/10229346
; Publication No. US20030120054A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Eric
; APPLICANT: Stacy, Cheryl
; TITLE OF INVENTION: Modified Cry3A Toxins
; FILE REFERENCE: 60065A
; CURRENT APPLICATION NUMBER: US/10/229,346
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/316,421
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(4)
; OTHER INFORMATION: Protease recognition sequence
US-10-229-346-35

```

```

Query Match          100.0%; Score 4; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 AAPF 4
        ||||
Db      1 AAPF 4

```

RESULT 13

```

US-09-994-927-1
; Sequence 1, Application US/09994927
; Patent No. US20020127605A1
; GENERAL INFORMATION:
; APPLICANT: Guilford Pharmaceuticals Inc.
; APPLICANT: Hamilton, Gregory
; APPLICANT: Belyakov, Sergei
; APPLICANT: Vaal, Mark
; APPLICANT: Wei, Ling
; APPLICANT: Wu, Yong-Qian
; APPLICANT: Steiner, Joseph
; TITLE OF INVENTION: Bisubstituted Carbocyclic Cyclophilin Binding Compounds
and Their Use
; FILE REFERENCE: 03166.0029.NPUS02
; CURRENT APPLICATION NUMBER: US/09/994,927
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/253,074
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/291,966
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 6

```

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Model substrate for measuring rotamase inhibition
activity
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa at position 1 is N-succinyl
; NAME/KEY: MISC_FEATURE
; LOCATION: (6)..(6)
; OTHER INFORMATION: Xaa at position 6 is p-nitroanilide
US-09-994-927-1

```

```

Query Match          100.0%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 AAPF 4
        ||||
Db      2 AAPF 5

```

RESULT 14

US-10-033-526-4

```

; Sequence 4, Application US/10033526
; Publication No. US20020147999A1
; GENERAL INFORMATION:
; APPLICANT: Robert W. Mahley
; APPLICANT: Yadong Huang
; TITLE OF INVENTION: Methods of Treating Disorders Related to
; TITLE OF INVENTION: APOE
; FILE REFERENCE: UCAL217
; CURRENT APPLICATION NUMBER: US/10/033,526
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 60/245,737
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-033-526-4

```

```

Query Match          100.0%; Score 4; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 AAPF 4
        ||||
Db      3 AAPF 6

```

RESULT 15

US-09-842-543-1

```

; Sequence 1, Application US/09842543
; Patent No. US20020010315A1
; GENERAL INFORMATION:
; APPLICANT: Gyorkos, et al.
; TITLE OF INVENTION: PEPTOID AND NONPEPTOID CONTAINING
; TITLE OF INVENTION: ALPHA-KETO SERINE PROTEASE INHIBITORS
; FILE REFERENCE: 361239-016A
; CURRENT APPLICATION NUMBER: US/09/842,543
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 09/325,512
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is a known commercially available
; OTHER INFORMATION: substrate for elastases.
; NAME/KEY: BLOCKED
; LOCATION: (1)...(1)
; OTHER INFORMATION: N-terminal Methoxysuccinyl group.
; NAME/KEY: BLOCKED
; LOCATION: (4)...(4)
; OTHER INFORMATION: C-terminal p-nitroaniline
US-09-842-543-1

```

```

Query Match          75.0%; Score 3; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 AAP 3
        |||
Db      1 AAP 3

```

```

Search completed: December 30, 2003, 12:36:15
Job time : 20.2857 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 12:19:51 ; Search time 9.42857 Seconds
(without alignments)
40.799 Million cell updates/sec

Title: US-10-033-526-1
Perfect score: 4
Sequence: 1 AAPF 4

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 293

Minimum DB seq length: 4

Maximum DB seq length: 6

Post-processing: Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	4	100.0	5	2		JS0319	subesophageal gang
2	3	75.0	6	2		B60110	repetitive protein
3	2	50.0	4	2		A34626	RPCH-related neuro
4	2	50.0	5	2		B41225	copper resistance
5	2	50.0	5	2		B60274	major protein anti
6	2	50.0	5	2		PS0324	ribulose-bisphosph
7	2	50.0	5	2		S55237	zinc-binding prote
8	2	50.0	5	2		G37196	bradykinin-potenti
9	2	50.0	5	2		S11127	phosphoprotein, bo
10	2	50.0	6	2		S66195	alcohol dehydrogen
11	2	50.0	6	2		A61049	halo-toxin - Pseud
12	2	50.0	6	2		C22565	R-phycoerythrin be
13	2	50.0	6	2		A43766	28K ubiquitin-immu

14	2	50.0	6	2	B27696	contraction-inhibi
15	2	50.0	6	2	I51317	bHLH transcription
16	2	50.0	6	2	PT0280	Ig heavy chain CRD
17	2	50.0	6	2	PT0616	T-cell receptor be
18	2	50.0	6	4	S15596	orf 3 rara 5'-regi
19	1	25.0	4	1	ECXAA	antho-RFamide neur
20	1	25.0	4	2	S18401	thyroglobulin - do
21	1	25.0	4	2	A02147	phagocytosis-stimu
22	1	25.0	4	2	A32039	tyrosine-melanocyt
23	1	25.0	4	2	ECNK	cardioexcitatory n
24	1	25.0	4	2	PL0140	carbon-monoxide de
25	1	25.0	4	2	PL0146	carbon-monoxide de
26	1	25.0	4	2	A48360	gamma subunit of P
27	1	25.0	4	2	S43014	hypothetical prote
28	1	25.0	4	2	D41654	hypothetical prote
29	1	25.0	4	2	S53508	starvation-induced
30	1	25.0	4	2	S17255	ribosomal protein
31	1	25.0	4	2	A27897	glucan 1,4-alpha-g
32	1	25.0	4	2	JQ1273	neuropeptide Antho
33	1	25.0	4	2	A35779	neuropeptide Antho
34	1	25.0	4	2	A25844	autho-RF amide neu
35	1	25.0	4	2	A60418	FMRFamide - polych
36	1	25.0	4	2	A32480	achatin-I - giant
37	1	25.0	4	2	I51049	metallothionein-A
38	1	25.0	4	2	S39390	myosin-light-chain
39	1	25.0	4	2	I61883	protamine P1 - ora
40	1	25.0	4	2	PT0240	Ig heavy chain CRD
41	1	25.0	4	2	PT0271	Ig heavy chain CRD
42	1	25.0	4	2	S43959	Ig mu chain V regi
43	1	25.0	4	2	I54357	schwannomin - mous
44	1	25.0	4	2	PT0696	T-cell receptor be
45	1	25.0	4	2	PT0645	T-cell receptor be

ALIGNMENTS

RESULT 1

JS0319

subesophageal ganglion pentapeptide - house cricket

C;Species: Acheta domesticus (house cricket)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000

C;Accession: JS0319

R;Wicker, C.; Wicker, C.

Comp. Biochem. Physiol. C 88, 185-187, 1987

A;Title: Isolation and structure of a peptide isolated from the subesophageal ganglion of Acheta domesticus (orthoptera).

A;Reference number: JS0319

A;Accession: JS0319

A;Molecule type: protein

A;Residues: 1-5 <WIC>

Query Match 100.0%; Score 4; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4

Db

||||
2 AAPF 5

RESULT 2

B60110

repetitive protein antigen 61 - Trypanosoma cruzi (fragment)

C;Species: Trypanosoma cruzi

C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 18-Jun-1993

C;Accession: B60110

R;Hoft, D.F.; Kim, K.S.; Otsu, K.; Moser, D.R.; Yost, W.J.; Blumin, J.H.;
Donelson, J.E.; Kirchhoff, L.V.

Infect. Immun. 57, 1959-1967, 1989

A;Title: Trypanosoma cruzi expresses diverse repetitive protein antigens.

A;Reference number: A60110; MUID:89277508; PMID:2659529

A;Accession: B60110

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-6 <HOF>

A;Note: this is an example of a five residue tandem repeat from this protein;
the actual protein sequence is not given in the paper

C;Keywords: tandem repeat

Query Match 75.0%; Score 3; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAP 3

Db 1 AAP 3

RESULT 3

A34626

RPCH-related neuropeptide - ferruginous spindle

C;Species: Fusinus ferrugineus (ferruginous spindle)

C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993

C;Accession: A34626

R;Kuroki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.;
Minamitake, Y.; Muneoka, Y.

Biochem. Biophys. Res. Commun. 167, 273-279, 1990

A;Title: A molluscan neuropeptide related to the crustacean hormone, RPCH.

A;Reference number: A34626; MUID:90179762; PMID:2310394

A;Accession: A34626

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-4 <KUR>

C;Keywords: neuropeptide

Query Match 50.0%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AP 3

Db 1 AP 2

RESULT 4

B41225

copper resistance protein B - *Pseudomonas syringae* pv. tomato (fragment)

C;Species: *Pseudomonas syringae* pv. tomato

C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993

C;Accession: B41225

R;Cha, J.S.; Cooksey, D.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991

A;Title: Copper resistance in *Pseudomonas syringae* mediated by periplasmic and outer membrane proteins.

A;Reference number: A41225; MUID:92020961; PMID:1924351

A;Accession: B41225

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-5 <CHA>

Query Match 50.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AA 2

||

Db 3 AA 4

RESULT 5

B60274

major protein antigen MPT32 - *Mycobacterium tuberculosis* (fragment)

C;Species: *Mycobacterium tuberculosis*

C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993

C;Accession: B60274

R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.

Infect. Immun. 59, 372-382, 1991

A;Title: Isolation and partial characterization of major protein antigens in the culture fluid of *Mycobacterium tuberculosis*.

A;Reference number: A60274; MUID:91099989; PMID:1898899

A;Accession: B60274

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-5 <NAG>

Query Match 50.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AP 3

||

Db 3 AP 4

RESULT 6

PS0324

ribulose-bisphosphate carboxylase activase III - rice (strain Nihonbare) (fragment)

C;Species: *Oryza sativa* (rice)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 02-Jul-1998

C;Accession: PS0324
R;Tsugita, A.
submitted to JIPID, April 1993
A;Reference number: PS0206
A;Accession: PS0324
A;Molecule type: protein
A;Residues: 1-5 <TSU>
A;Experimental source: leaf, chlorophyll

Query Match 50.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AP 3
||
Db 3 AP 4

RESULT 7

S55237
zinc-binding protein ZBP14 - maize (fragment)
C;Species: Zea mays (maize)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C;Accession: S55237
R;Robinson, K.; Jones, D.; Howell, S.; Soneji, Y.; Martin, S.; Aitken, A.
Biochem. J. 307, 267-272, 1995
A;Title: Expression and characterization of maize ZBP14, a member of a new
family of zinc-binding proteins.
A;Reference number: S55237; MUID:95234046; PMID:7717986
A;Accession: S55237
A;Molecule type: protein
A;Residues: 1-5 <ROB>

Query Match 50.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AA 2
||
Db 2 AA 3

RESULT 8

G37196
bradykinin-potentiating peptide 7 - island jararaca
C;Species: Bothrops insularis (island jararaca)
C;Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C;Accession: G37196
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A;Title: Primary structure and biological activity of bradykinin potentiating
peptides from Bothrops insularis snake venom.
A;Reference number: A37196; MUID:90351557; PMID:2386615
A;Accession: G37196
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <CIN>

C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 50.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AP 3
||
Db 4 AP 5

RESULT 9

S11127

phosphoprotein, bone - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Mar-2000

C;Accession: S11127; S11128

R;Mikuni-Takagaki, Y.; Glimcher, M.J.

Biochem. J. 268, 585-591, 1990

A;Title: Post-translational processing of chicken bone phosphoproteins.
Identification of the bone phosphoproteins of embryonic tibia.

A;Reference number: S11127; MUID:90303246; PMID:2363696

A;Accession: S11127

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-5 <MIK1>

A;Accession: S11128

A;Status: preliminary

A;Molecule type: protein

A;Residues: 'X',2-5 <MIK2>

C;Keywords: phosphoprotein

Query Match 50.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AP 3
||
Db 1 AP 2

RESULT 10

S66195

alcohol dehydrogenase (EC 1.1.1.1) class III low affinity form - cod (Gadus sp.)
(fragment)

C;Species: Gadus sp. (cod)

C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 12-Jun-1998

C;Accession: S66195

R;Hjelmqvist, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.;

Hendrickson, R.C.; Michel, H.; Shabanowitz, J.; Hunt, D.F.; Joernvall, H.

FEBS Lett. 367, 237-240, 1995

A;Title: Multiplicity of N-terminal structures of medium-chain alcohol
dehydrogenases. Mass-spectrometric analysis of plant, lower vertebrate and
higher vertebrate class I, II, and III forms of the enzyme.

A;Reference number: S66191; MUID:95331382; PMID:7607314

A;Accession: S66195

A;Molecule type: protein
A;Residues: 1-6 <HJE>
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 50.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AA 2
||
Db 1 AA 2

RESULT 11

A61049

halo-toxin - *Pseudomonas syringae* pv. *mori*

C;Species: *Pseudomonas syringae* pv. *mori*

A;Note: host mulberry tree

C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 21-Jan-1997

C;Accession: A61049

R;Kajimoto, T.; Yokomizo, K.; Yahiro, K.; Umeda, T.; Shoji, S.; Kubota, Y.;
Shibata, M.; Takahashi, K.; Nohara, T.

Chem. Lett. 00, 679-680, 1989

A;Title: Structure of halo-toxin produced by phytopathogenic bacterium,
Pseudomonas syringae pv. *mori*.

A;Reference number: A61049

A;Accession: A61049

A;Molecule type: protein

A;Residues: 1-6 <KAJ>

A;Note: sequence confirmed by synthesis

C;Comment: This toxin is one of the etiological agents of halo bright disease in
mulberry tress.

C;Keywords: toxin

Query Match 50.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PF 4
||
Db 1 PF 2

RESULT 12

C22565

R-phycoerythrin beta-1 chain - red alga (*Gastroclonium coulteri*) (fragment)

C;Species: *Gastroclonium coulteri*

C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993

C;Accession: C22565

R;Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985

A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.

A;Reference number: A22565; MUID:85182601; PMID:3886644

A;Accession: C22565

A;Molecule type: protein

A;Residues: 1-6 <KLO>

Query Match 50.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AA 2
||
Db 2 AA 3

RESULT 13

A43766

28K ubiquitin-immunoreactive protein - inky cap (*Coprinus cinereus*) (fragment)

C;Species: *Coprinus cinereus*

C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 30-Sep-1993

C;Accession: A43766

R;Kanda, T.; Inoue, M.; Akiyama, M.

Biochimie 72, 355-359, 1990

A;Title: Purification and characterization of an ubiquitin-immuno-reactive protein localized in the cap of young basidiocarp in the basidiomycete *Coprinus cinereus*.

A;Reference number: A43766; MUID:91002724; PMID:1698461

A;Accession: A43766

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-6 <KAN>

Query Match 50.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AP 3
||
Db 1 AP 2

RESULT 14

B27696

contraction-inhibiting peptide II - blue mussel

C;Species: *Mytilus edulis* (blue mussel)

C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 08-Dec-1995

C;Accession: B27696

R;Hirata, T.; Kubota, I.; Iwasawa, N.; Takabatake, I.; Ikeda, T.; Muneoka, Y.

Biochem. Biophys. Res. Commun. 152, 1376-1382, 1988

A;Title: Structures and actions of *Mytilus* inhibitory peptides.

A;Reference number: A90142; MUID:88240357; PMID:3377776

A;Accession: B27696

A;Molecule type: protein

A;Residues: 1-6 <HIR>

C;Keywords: amidated carboxyl end

F;6/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 50.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AP 3

Db ||
 2 AP 3

RESULT 15

I51317

bHLH transcription factor inhibitor - African clawed frog (fragment)

C;Species: Xenopus laevis (African clawed frog)

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C;Accession: I51317

R;Zhang, H.; Reynaud, S.; Kloc, M.; Etkin, L.D.; Spohr, G.

Mech. Dev. 50, 119-130, 1995

A;Title: Id gene activity during Xenopus embryogenesis.

A;Reference number: I51316; MUID:95344988; PMID:7619724

A;Accession: I51317

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-6 <ZHA>

A;Cross-references: GB:S79038; NID:gl042006; PIDN:AAD14294.1; PID:g4261994

C;Genetics:

A;Gene: XIdIb

Query Match 50.0%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PF 4

||

Db 5 PF 6

Search completed: December 30, 2003, 12:24:27

Job time : 10.4286 secs

OM protein - protein search, using sw model

Run on: December 30, 2003, 12:16:41 ; Search time 6.57143 Seconds
 (without alignments)
 28.625 Million cell updates/sec

Title: US-10-033-526-1
 Perfect score: 4
 Sequence: 1 AAPF 4

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 47

Minimum DB seq length: 4
 Maximum DB seq length: 6

Post-processing: Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	4	100.0	5	1	SUGA_ACHDO	P19991 acheta dome
2	2	50.0	5	1	BPP7_BOTIN	P30425 bothrops in
3	2	50.0	6	1	CIP2_MYTED	P13737 mytilus edu
4	1	25.0	4	1	ACH1_ACHFU	P35904 achatina fu
5	1	25.0	4	1	DCML_PSECH	P19916 pseudomonas
6	1	25.0	4	1	DCMS_PSECH	P19918 pseudomonas
7	1	25.0	4	1	FAR3_HIRME	P42562 hirudo medi
8	1	25.0	4	1	FAR4_HIRME	P42563 hirudo medi
9	1	25.0	4	1	FFKA_ANTEL	P58705 anthopleura
10	1	25.0	4	1	FLRF_HIRME	P42561 hirudo medi
11	1	25.0	4	1	FLRN_ANTEL	P58707 anthopleura
12	1	25.0	4	1	FMRF_MACNI	P01162 macrocallis
13	1	25.0	4	1	FYRI_ANTEL	P58706 anthopleura
14	1	25.0	4	1	OCP1_OCTMI	P58648 octopus min
15	1	25.0	4	1	RM01_YEAST	P36515 saccharomyc
16	1	25.0	4	1	TUFT_HUMAN	P01858 homo sapien
17	1	25.0	5	1	AL14_CARMA	P81817 carcinus ma

18	1	25.0	5	1	BIOB_CITFR	P12997	citrobacter
19	1	25.0	5	1	EI03_LITRU	P82099	litoria rub
20	1	25.0	5	1	EI04_LITRU	P82100	litoria rub
21	1	25.0	5	1	FARP_ARTTR	P41853	artioposthi
22	1	25.0	5	1	PAP2_PARMA	P81864	pardachirus
23	1	25.0	5	1	PRCT_PERAM	P01373	periplaneta
24	1	25.0	5	1	RE11_LITRU	P82070	litoria rub
25	1	25.0	5	1	RE21_LITRU	P82071	litoria rub
26	1	25.0	5	1	RE31_LITRU	P82072	litoria rub
27	1	25.0	5	1	RE32_LITRU	P82073	litoria rub
28	1	25.0	5	1	TPIS_CANFA	P54714	canis famil
29	1	25.0	5	1	UC22_MAIZE	P80628	zea mays (m
30	1	25.0	6	1	CIP1_MYTED	P13736	mytilus edu
31	1	25.0	6	1	EI01_LITRU	P82096	litoria rub
32	1	25.0	6	1	FARP_MONEX	P41966	moniezia ex
33	1	25.0	6	1	LOK1_LOCFI	P41491	locusta mig
34	1	25.0	6	1	OVM_LEPDE	P42985	leptinotars
35	1	25.0	6	1	TMOF_SARBU	P41495	sarcophaga
36	1	25.0	6	1	TRPI_PSEPU	P36414	pseudomonas
37	1	25.0	6	1	UN06_CLOPA	P81351	clostridium
38	1	25.0	6	1	VP19_HSV1K	P23210	herpes simp
39	0	0.0	4	1	EOSI_HUMAN	P02731	homo sapien
40	0	0.0	4	1	OCP3_OCTMI	P58649	octopus min
41	0	0.0	5	1	BIOA_CITFR	P13071	citrobacter
42	0	0.0	5	1	PSK_DAUCA	P58261	daucus caro
43	0	0.0	5	1	TRM3_ECOLI	P13973	escherichia
44	0	0.0	5	1	UF01_MOUSE	P38639	mus musculu
45	0	0.0	5	1	UXA4_CHLTR	P38005	chlamydia t

ALIGNMENTS

RESULT 1

SUGA_ACHDO

ID SUGA_ACHDO STANDARD; PRT; 5 AA.

AC P19991;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Suboesophageal ganglion pentapeptide.

OS Acheta domesticus (House cricket).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;

OC Acheta.

OX NCBI_TaxID=6997;

RN [1]

RP SEQUENCE.

RA Wicker C., Wicker C.;

RT "Isolation and structure of a peptide isolated from the

RT suboesophageal ganglion of Acheta domesticus (orthoptera).";

RL Comp. Biochem. Physiol. 88C:185-187(1987).

CC -!- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBOESOPHAGEAL

CC GLANDIA.

DR PIR; JS0319; JS0319.

SQ SEQUENCE 5 AA; 476 MW; 69D76DDDDDB00000 CRC64;

Query Match 100.0%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPF 4
|||
Db 2 AAPF 5

RESULT 2

BPP7_BOTIN

ID BPP7_BOTIN STANDARD; PRT; 5 AA.
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom."
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; G37196; G37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AP 3
||
Db 4 AP 5

RESULT 3

CIP2_MYTED

ID CIP2_MYTED STANDARD; PRT; 6 AA.
AC P13737;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Contraction-inhibiting peptide II (MIP II).

OS *Mytilus edulis* (Blue mussel).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
 OC Mytiloidea; Mytilidae; Mytilus.
 OX NCBI_TaxID=6550;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pedal ganglion;
 RX MEDLINE=88240357; PubMed=3377776;
 RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
 RT "Structures and actions of *Mytilus* inhibitory peptides.";
 RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
 CC -!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
 CC MUSCLES.
 CC -!- SIMILARITY: TO MIP I.
 DR PIR; B27696; B27696.
 KW Hormone; Amidation.
 FT MOD_RES 6 6 AMIDATION.
 SQ SEQUENCE 6 AA; 621 MW; 72C9C6876DD81000 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AP 3
 ||
 Db 2 AP 3

RESULT 4

ACH1_ACHFU

ID ACH1_ACHFU STANDARD; PRT; 4 AA.
 AC P35904;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Achatin-I.
 OS *Achatina fulica* (Giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
 RC STRAIN=Ferussac; TISSUE=Ganglion;
 RX MEDLINE=89273551; PubMed=2597281;
 RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
 RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
 RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
 RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from *Achatina*
 RT *fulica* Ferussac containing a D-amino acid residue.";
 RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
 RN [2]
 RP CHARACTERIZATION.
 RC STRAIN=Ferussac; TISSUE=Heart atrium;
 RX MEDLINE=91264856; PubMed=1675568;
 RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
 RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
 RT "Purification of achatin-I from the atria of the African giant snail,

RT Achatina fulica, and its possible function.";
 RL Biochem. Biophys. Res. Commun. 177:847-853(1991).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=93014529; PubMed=1399265;
 RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
 RA Iwashita T., Nomoto K.;
 RT "Crystal structure and molecular conformation of achatin-I
 RT (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
 RT D-amino acid residue.";
 RL Int. J. Pept. Protein Res. 39:258-264(1992).
 CC -!- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY
 CC AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY
 CC NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE
 CC HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.
 DR PIR; A32480; A32480.
 KW Hormone; D-amino acid.
 FT MOD_RES 2 2 D-PHENYLALANINE.
 SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;

Query Match 25.0%; Score 1; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 F 4
 |
 Db 2 F 2

RESULT 5

DCML_PSECH

ID DCML_PSECH STANDARD; PRT; 4 AA.
 AC P19916;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO
 DE dehydrogenase subunit L) (CO-DH L) (Fragment).
 GN CUTL.
 OS Pseudomonas carboxydohydrogena.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae.
 OX NCBI_TaxID=290;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90055678; PubMed=2818128;
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 RT carboxydotrophic bacteria.";
 RL Arch. Microbiol. 152:335-341(1989).
 CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
 CC dioxide.
 CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
 CC acceptor.
 CC -!- COFACTOR: Molybdenum (molybdopterin).
 CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 CC SMALL.

DR PIR; PL0140; PL0140.
KW Oxidoreductase; Molybdenum.
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;

Query Match 25.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 P 3
|
Db 4 P 4

RESULT 6

DCMS_PSECH
ID DCMS_PSECH STANDARD; PRT; 4 AA.
AC P19918;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO
DE dehydrogenase subunit S) (CO-DH S) (Fragment).
GN CUTS.
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae.
OX NCBI_TaxID=290;
RN [1]
RP SEQUENCE.
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
RT carboxydotrophic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
CC dioxide.
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
CC acceptor.
CC -!- COFACTOR: BINDS TWO 2FE-2S CLUSTERS.
CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC SMALL.
DR PIR; PL0146; PL0146.
KW Oxidoreductase; Metal-binding; Iron-sulfur; Iron; 2Fe-2S.
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 420 MW; 6DD33DD6F0000000 CRC64;

Query Match 25.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 2 A 2

RESULT 7

FAR3_HIRME

ID FAR3_HIRME STANDARD; PRT; 4 AA.
 AC P42562;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide YLRF-amide.
 OS Hirudo medicinalis (Medicinal leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92195954; PubMed=1686933;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech."
 RL Peptides 12:897-908(1991).
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 4 4 AMIDATION.
 SQ SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;

Query Match 25.0%; Score 1; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 F 4
 |
 Db 4 F 4

RESULT 8

FAR4_HIRME

ID FAR4_HIRME STANDARD; PRT; 4 AA.
 AC P42563;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide YMRF-amide.
 OS Hirudo medicinalis (Medicinal leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92195954; PubMed=1686933;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech."
 RL Peptides 12:897-908(1991).
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 4 4 AMIDATION.
 SQ SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;

Query Match 25.0%; Score 1; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 F 4
|
Db 4 F 4

RESULT 9

FFKA_ANTEL

ID FFKA_ANTEL STANDARD; PRT; 4 AA.
AC P58705;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Antho-KAamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Chidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynantheae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE.
RX MEDLINE=92028852; PubMed=1681803;
RA Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
RT "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH₂ (Antho-KAamide), a
RT novel neuropeptide from sea anemones."
RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
RN [2]
RP FUNCTION.
RX MEDLINE=93391436; PubMed=8397415;
RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
RT inhibitory neuropeptides, Antho-KAamide and Antho-RIamide."
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Neuron-specific.
DR PIR; JQ1273; JQ1273.
KW Neuropeptide; Amidation.
FT MOD_RES 1 1 L-3-PHENYLLACTYL.
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 512 MW; 6DD339C9A0000000 CRC64;

Query Match 25.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 F 4
|
Db 1 F 1

RESULT 10

FLRF_HIRME

ID FLRF_HIRME STANDARD; PRT; 4 AA.

AC P42561;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FLRFamide.
 OS *Hirudo medicinalis* (Medicinal leech), and
 OS *Helisoma trivolvis* (Snail).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Arynchobdellida; Hirudiniformes; Hirudinidae; *Hirudo*.
 OX NCBI_TaxID=6421, 27815;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=*H.medicinalis*;
 RX MEDLINE=92195954; PubMed=1686933;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech."
 RL Peptides 12:897-908(1991).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=*H.trivolvis*; TISSUE=Kidney;
 RX MEDLINE=94286417; PubMed=7912428;
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
 RT "FMRFamide-related peptides from the kidney of the snail, *Helisoma*
 RT *trivolvis*."
 RL Peptides 15:31-36(1994).
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 4 4 AMIDATION.
 SQ SEQUENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;

Query Match 25.0%; Score 1; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 F 4
 |
 Db 1 F 1

RESULT 11
 FLRN_ANTEL

ID FLRN_ANTEL STANDARD; PRT; 4 AA.
 AC P58707;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Antho-RNamide.
 OS *Anthopleura elegantissima* (Sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nynanthaeae; Actiniidae; *Anthopleura*.
 OX NCBI_TaxID=6110;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RX MEDLINE=90319122; PubMed=1973541;
 RA Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
 RA Reinscheid R.K., Nothacker H.-P., Staley A.L.;

RT "Isolation of L-3-phenyllactyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea
RT anemone neuropeptide containing an unusual amino-terminal blocking
RT group.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Neuron-specific.
CC -!- MASS SPECTROMETRY: MW=549.3; METHOD=FAB.
DR PIR; A35779; A35779.
KW Neuropeptide; Amidation.
FT MOD_RES 1 1 L-3-PHENYLLACTYL.
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 549 MW; 64540729A0000000 CRC64;

Query Match 25.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 F 4
|
Db 1 F 1

RESULT 12

FMRF_MACNI

ID FMRF_MACNI STANDARD; PRT; 4 AA.
AC P01162;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE FMRFamide (Peak C) (Cardioexcitatory neuropeptide).
OS Macrocallista nimbosa (Sun-ray clam),
OS Nereis virens (Sandworm),
OS Hirudo medicinalis (Medicinal leech), and
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;
OC Veneroidea; Veneridae; Macrocallista.
OX NCBI_TaxID=6594, 6353, 6421, 27815;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC SPECIES=M.nimbosa; TISSUE=Cerebral pedal, and Visceral ganglion;
RX MEDLINE=77215956; PubMed=877582;
RA Price D.A., Greenberg M.J.;
RT "Structure of a molluscan cardioexcitatory neuropeptide.";
RL Science 197:670-671(1977).
RN [2]
RP SEQUENCE, AND CHARACTERIZATION.
RC SPECIES=M.nimbosa; TISSUE=Ganglion;
RX MEDLINE=78012038; PubMed=909875;
RA Price D.A., Greenberg M.J.;
RT "Purification and characterization of a cardioexcitatory neuropeptide
RT from the central ganglia of a bivalve mollusc.";
RL Prep. Biochem. 7:261-281(1977).
RN [3]
RP SEQUENCE.
RC SPECIES=N.virens;
RX MEDLINE=90259866; PubMed=2342992;
RA Krajniak K.G., Price D.A.;

RT "Authentic FMRFamide is present in the polychaete *Nereis virens*.";
 RL Peptides 11:75-77(1990).
 RN [4]
 RP SEQUENCE.
 RC SPECIES=*H. medicinalis*;
 RX MEDLINE=92195954; PubMed=1686933;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech.";
 RL Peptides 12:897-908(1991).
 RN [5]
 RP SEQUENCE.
 RC SPECIES=*H. trivolvis*; TISSUE=Kidney;
 RX MEDLINE=94286417; PubMed=7912428;
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
 RT "FMRFamide-related peptides from the kidney of the snail, *Helisoma*
 RT *trivolvis*.";
 RL Peptides 15:31-36(1994).
 CC -!- FUNCTION: MYOACTIVE; CARDIOEXCITATORY SUBSTANCE. PHARMACOLOGICAL
 CC ACTIVITIES INCLUDE AUGMENTATION, INDUCTION, AND REGULARIZATION OF
 CC CARDIAC CONTRACTION.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 DR PIR; A01426; ECKN.
 DR PIR; A60418; A60418.
 KW Neuropeptide; Amidation.
 FT MOD RES 4 4 AMIDATION.
 SQ SEQUENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;

Query Match 25.0%; Score 1; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 F 4
 |
 Db 1 F 1

RESULT 13

FYRI_ ANTEL

ID FYRI_ ANTEL STANDARD; PRT; 4 AA.
 AC P58706;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Antho-RIamide I [Contains: Antho-RIamide II].
 OS Anthopleura elegantissima (Sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nynantheae; Actiniidae; Anthopleura.
 OX NCBI_TaxID=6110;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92270459; PubMed=1821096;
 RA Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D.,
 RA Grimmelikhuijzen C.J.P.;
 RT "Isolation of two novel neuropeptides from sea anemones: the unusual,
 RT biologically active L-3-phenyllactyl-Tyr-Arg-Ile-NH2 and its
 RT des-phenyllactyl fragment Tyr-Arg-Ile-NH2.";

RL Peptides 12:1165-1173(1991).
 RN [2]
 RP FUNCTION.
 RX MEDLINE=93391436; PubMed=8397415;
 RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmlikhuijzen C.J.P.;
 RT "The expansion behaviour of sea anemones may be coordinated by two
 RT inhibitory neuropeptides, Antho-KAamide and Antho-RIamide.";
 RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
 CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle
 CC groups. May be involved in the expansion phase of feeding
 CC behaviour in sea anemones.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Neuron-specific.
 KW Neuropeptide; Amidation.
 FT CHAIN 1 4 ANTHO-RIAMIDE I.
 FT CHAIN 2 4 ANTHO-RIAMIDE II.
 FT MOD_RES 1 1 L-3-PHENYLLACTYL.
 FT MOD_RES 4 4 AMIDATION.
 SQ SEQUENCE 4 AA; 598 MW; 60441B59A0000000 CRC64;

 Query Match 25.0%; Score 1; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 F 4
 |
 Db 1 F 1

RESULT 14

OCP1_OCTMI
 ID OCP1_OCTMI STANDARD; PRT; 4 AA.
 AC P58648;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cardioactive peptides Ocp-1/Ocp-2.
 OS Octopus minor (Octopus).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
 OX NCBI_TaxID=89766;
 RN [1]
 RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
 RC TISSUE=Brain;
 RX MEDLINE=20336815; PubMed=10876044;
 RA Iwakoshi E., Hisada M., Minakata H.;
 RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
 RT Octopus minor.";
 RL Peptides 21:623-630(2000).
 CC -!- FUNCTION: Cardioactive; has both positive chronotropic and
 CC inotropic effects on the heart. Ocp-2 is a 1000 time less
 CC active than Ocp-1.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PTM: Ocp-2 has L-Phe instead of D-Phe.
 CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
 KW Hormone; D-amino acid.
 FT MOD_RES 2 2 D-PHENYLALANINE.

SQ SEQUENCE 4 AA; 394 MW; 6AA879C810000000 CRC64;

Query Match 25.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 F 4
|
Db 2 F 2

RESULT 15

RM01_YEAST

ID RM01_YEAST STANDARD; PRT; 4 AA.
AC P36515;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Mitochondrial 60S ribosomal protein L1 (YmL1) (Fragment).
GN MRPL1.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RX MEDLINE=91285106; PubMed=2060626;
RA Grohmann L., Graack H.-R., Kruft V., Choli T., Goldschmidt-Reisin S.,
RA Kitakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal
RT subunit from yeast mitochondria."
RL FEBS Lett. 284:51-56(1991).
DR PIR; S17255; S17255.
DR SGD; L0002681; MRPL1.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000 CRC64;

Query Match 25.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 P 3
|
Db 4 P 4

Search completed: December 30, 2003, 12:23:40
Job time : 7.57143 secs

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OM protein - protein search, using sw model

Run on: December 30, 2003, 12:20:27 ; Search time 22.8571 Seconds
(without alignments)
45.159 Million cell updates/sec

Title: US-10-033-526-1
Perfect score: 4
Sequence: 1 AAPF 4

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 4
Maximum DB seq length: 6

Post-processing: Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Query	Length	DB	ID	Description
No.							

1	1	25.0	5	10	Q99007	Q99007 hordeum vul
2	1	25.0	5	13	P83308	P83308 gallus gall
3	1	25.0	6	10	P82181	P82181 spinacia ol
4	1	25.0	6	10	P82182	P82182 spinacia ol
5	0	0.0	4	11	Q08433	Q08433 rattus sp.
6	0	0.0	5	2	P83073	P83073 bacillus ce
7	0	0.0	6	10	P82541	P82541 spinacia ol

ALIGNMENTS

RESULT 1

Q99007

ID Q99007 PRELIMINARY; PRT; 5 AA.
AC Q99007;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Alpha amylase (Fragment).
GN AMY1 GENE.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91329704; PubMed=1831055;
RA Jacobsen J.V., Close T.J.;
RT "Control of transient expression of chimaeric genes by gibberellic
RT acid and abscisic acid in protoplasts prepared from mature barley
RT aleurone layers.";
RL Plant Mol. Biol. 16:713-721(1991).
DR EMBL; X54643; CAA38455.1; -.
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;

Query Match 25.0%; Score 1; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 2 A 2

RESULT 2

P83308

ID P83308 PRELIMINARY; PRT; 5 AA.
AC P83308;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE FMRFamide-like neuropeptide (LPLRF-amide).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Brain;
 RX PubMed=6137771;
 RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
 RT "A novel active pentapeptide from chicken brain identified by
 RT antibodies to FMRFamide.";
 RL Nature 305:328-330(1983).
 CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide.
 SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 25.0%; Score 1; DB 13; Length 5;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 P 3
 |
 Db 2 P 2

RESULT 3

P82181

ID P82181 PRELIMINARY; PRT; 6 AA.
 AC P82181;
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Chloroplast 50S ribosomal protein L10 beta (Fragment).
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. ALWARO; TISSUE=Leaf;
 RX MEDLINE=20435798; PubMed=10874046;
 RA Yamaguchi K., Subramanian A.R.;
 RT "The plastid ribosomal proteins. Identification of all the proteins in
 RT the 50 S subunit of an organelle ribosome (chloroplast).";
 RL J. Biol. Chem. 275:28466-28482(2000).
 CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
 CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro; IPR001790; Ribosomal_L10.
 DR InterPro; IPR002363; Ribosomal_L10eub.
 DR Pfam; PF00466; Ribosomal_L10; PARTIAL.
 DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.

FT NON_TER 6 6
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 25.0%; Score 1; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 1 A 1

RESULT 4

P82182

ID P82182 PRELIMINARY; PRT; 6 AA.
AC P82182;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Chloroplast 50S ribosomal protein L10 gamma (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. ALWARO; TISSUE=Leaf;
RX MEDLINE=20435798; PubMed=10874046;
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro; IPR001790; Ribosomal_L10.
DR InterPro; IPR002363; Ribosomal_L10eub.
DR Pfam; PF00466; Ribosomal_L10; PARTIAL.
DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 25.0%; Score 1; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 1 A 1

RESULT 5

Q08433

ID Q08433 PRELIMINARY; PRT; 4 AA.
AC Q08433;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Bilirubin UDP-glucuronosyltransferase (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gunn;
RX MEDLINE=91282758; PubMed=1840486;
RA Sato H., Aono S., Kashiwamata S., Koiwai O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
RT hyperbilirubinemic Gunn rat.";
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
DR EMBL; S38636; AAB19259.1; -.
KW Transferase.
FT NON_TER 1 1
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 0.0%; Score 0; DB 11; Length 4;
Best Local Similarity 0.0%; Pred. No. 8.3e+05;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 A 1

Db 1 N 1

RESULT 6

P83073

ID P83073 PRELIMINARY; PRT; 5 AA.
AC P83073;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE 88 kDa protein (Fragment).
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE.
RC STRAIN=NCIMB 11796;
RA Browne N., Dowds B.C.A.;
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;

Query Match 0.0%; Score 0; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 8.3e+05;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 A 1

Db 1 M 1

RESULT 7

P82541

ID P82541 PRELIMINARY; PRT; 6 AA.
AC P82541;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Chloroplast 30S ribosomal protein S19 beta (Fragment).
OS Spinacia oleracea (Spinach).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC STRAIN=cv. ALWARO; TISSUE=Leaf;
RX MEDLINE=20435797; PubMed=10874039;
RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the small subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 37:28455-28465(2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.
CC -!- MASS SPECTROMETRY: MW=10495; METHOD=MALDI.
CC -!- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PI. S19 BETA
CC FORM IS THE MINOR BASIC FORM.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 KDA.
CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro; IPR002222; Ribosomal_S19.
DR Pfam; PF00203; Ribosomal_S19; PARTIAL.
DR PRINTS; PR00975; RIBOSOMALS19; PARTIAL.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;

Query Match 0.0%; Score 0; DB 10; Length 6;
Best Local Similarity 0.0%; Pred. No. 8.3e+05;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 A 1

Db 1 T 1

Search completed: December 30, 2003, 12:25:59
Job time : 22.8571 secs

OM protein - protein search, using sw model

Run on: December 30, 2003, 12:21:17 ; Search time 10.5714 Seconds
 (without alignments)
 16.010 Million cell updates/sec

Title: US-10-033-526-3
 Perfect score: 4
 Sequence: 1 AAPL 4

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 36631

Minimum DB seq length: 4
 Maximum DB seq length: 6

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	4	100.0	4	1	US-08-004-643C-4
2	4	100.0	4	1	US-08-345-820B-1
3	4	100.0	4	1	US-08-544-143A-6
4	4	100.0	4	1	US-08-224-868-9
5	4	100.0	4	1	US-08-777-208-6
6	4	100.0	4	1	US-08-693-653-1
7	4	100.0	4	2	US-08-698-575E-1
8	4	100.0	4	2	US-08-907-840A-3
9	4	100.0	4	2	US-08-765-165-1
10	4	100.0	4	3	US-09-069-823-1
11	4	100.0	4	4	US-09-578-303-10

12	4	100.0	6	4	US-08-988-842-3	Sequence 3, Appli
13	3	75.0	4	1	US-07-943-848-1	Sequence 1, Appli
14	3	75.0	4	1	US-07-973-335-1	Sequence 1, Appli
15	3	75.0	4	1	US-08-155-331-18	Sequence 18, Appl
16	3	75.0	4	1	US-08-155-331-19	Sequence 19, Appl
17	3	75.0	4	1	US-08-323-418-2	Sequence 2, Appli
18	3	75.0	4	1	US-08-323-418-3	Sequence 3, Appli
19	3	75.0	4	1	US-08-004-643C-2	Sequence 2, Appli
20	3	75.0	4	1	US-08-004-643C-3	Sequence 3, Appli
21	3	75.0	4	1	US-08-004-643C-7	Sequence 7, Appli
22	3	75.0	4	1	US-08-166-316-7	Sequence 7, Appli
23	3	75.0	4	1	US-08-462-456-3	Sequence 3, Appli
24	3	75.0	4	1	US-08-462-456-5	Sequence 5, Appli
25	3	75.0	4	1	US-08-282-860-1	Sequence 1, Appli
26	3	75.0	4	1	US-08-407-000-6	Sequence 6, Appli
27	3	75.0	4	1	US-07-890-422B-28	Sequence 28, Appl
28	3	75.0	4	1	US-08-002-202-21	Sequence 21, Appl
29	3	75.0	4	1	US-08-276-936A-1	Sequence 1, Appli
30	3	75.0	4	1	US-08-276-936A-2	Sequence 2, Appli
31	3	75.0	4	1	US-08-345-820B-2	Sequence 2, Appli
32	3	75.0	4	1	US-08-345-820B-4	Sequence 4, Appli
33	3	75.0	4	1	US-08-544-143A-3	Sequence 3, Appli
34	3	75.0	4	1	US-08-544-143A-4	Sequence 4, Appli
35	3	75.0	4	1	US-08-544-143A-5	Sequence 5, Appli
36	3	75.0	4	1	US-08-544-143A-7	Sequence 7, Appli
37	3	75.0	4	1	US-08-544-143A-8	Sequence 8, Appli
38	3	75.0	4	1	US-08-544-143A-9	Sequence 9, Appli
39	3	75.0	4	1	US-08-544-143A-10	Sequence 10, Appl
40	3	75.0	4	1	US-08-544-143A-11	Sequence 11, Appl
41	3	75.0	4	1	US-08-544-143A-12	Sequence 12, Appl
42	3	75.0	4	1	US-08-544-143A-13	Sequence 13, Appl
43	3	75.0	4	1	US-08-544-143A-14	Sequence 14, Appl
44	3	75.0	4	1	US-08-544-143A-15	Sequence 15, Appl
45	3	75.0	4	1	US-08-544-143A-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1

US-08-004-643C-4

; Sequence 4, Application US/08004643C

; Patent No. 5480779

; GENERAL INFORMATION:

; APPLICANT: Gunter Fischer & Gerhard K llerz

; TITLE OF INVENTION: Cyclosporine Assay

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Gunter Fischer et al. c/o G. P. Katona

; STREET: 230 Park Avenue, Room 2200

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10169

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM pc compatible

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;   OPERATING SYSTEM:  MS-DOS
;   SOFTWARE:  conf. to PatentIn Release #1.0, Ver.#1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/004,643C
;     FILING DATE:  12 January 1993
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  703,590
;     FILING DATE:  20 May 1991
;     APPLICATION NUMBER:  398,092
;     FILING DATE:  24 August 1989
;     APPLICATION NUMBER:  DD WP 601 F/319 577W
;     FILING DATE:  07 September 1988
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Katona, Gabriel P.
;     REGISTRATION NUMBER:  20,829
;     REFERENCE/DOCKET NUMBER:  691-003
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (212)986-3377
;     TELEFAX:  (212)986-6126
;     TELEX:
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  4 amino acid residues
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-004-643C-4

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Query Match          100.0%;  Score 4;  DB 1;  Length 4;
Best Local Similarity 100.0%;  Pred. No. 2.5e+05;
Matches      4;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

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Qy      1 AAPL 4
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Db      1 AAPL 4

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RESULT 2

US-08-345-820B-1

; Sequence 1, Application US/08345820B

; Patent No. 5618792

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: SUBSTITUTED HETEROCYCLIC COMPOUNDS USEFUL AS

; TITLE OF INVENTION: INHIBITORS OF (SERINE PROTEASES) HUMAN NEUTROPHIL
ELASTASE

; NUMBER OF SEQUENCES: 4

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/345,820B

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-345-820B-1

Query Match 100.0%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
|||
Db 1 AAPL 4

RESULT 3

US-08-544-143A-6

; Sequence 6, Application US/08544143A
; Patent No. 5646028
; GENERAL INFORMATION:
; APPLICANT: Leigh, Scott D.
; TITLE OF INVENTION: NOVEL ALKALINE PROTEASE AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111-4121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/544,143A
; FILING DATE: 17-OCT-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: de Runtz, K. Alison
; REGISTRATION NUMBER: 37,119
; REFERENCE/DOCKET NUMBER: 0409.054US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-362-5556
; TELEFAX: 415-362-5418
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-544-143A-6

Query Match 100.0%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
 ||||
Db 1 AAPL 4

RESULT 4

US-08-224-868-9

; Sequence 9, Application US/08224868

; Patent No. 5698448

; GENERAL INFORMATION:

; APPLICANT: Soldin, Steven J.

; TITLE OF INVENTION: IMMUNOSUPPRESSIVE DRUG BINDING PROTEINS

; TITLE OF INVENTION: AND USE

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/224,868

; FILING DATE: 08-APR-1995

; CLASSIFICATION: 436

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/200,404

; FILING DATE: 23-FEB-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/782,761

; FILING DATE: 22-OCT-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/487,115

; FILING DATE: 02-MAR-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/279,176

; FILING DATE: 02-DEC-1988

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/841,792

; FILING DATE: 26-FEB-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/521,074

; FILING DATE: 09-MAY-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Bent, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 64688/125/CHRE

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-224-868-9

Query Match 100.0%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPL 4
|||
Db 1 AAPL 4

RESULT 5

US-08-777-208-6

; Sequence 6, Application US/08777208
; Patent No. 5763576
; GENERAL INFORMATION:
; APPLICANT: Powers, James C.
; TITLE OF INVENTION: Tetrapeptide Alpha-Ketoamides
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Deveau, Colton & Marquis
; STREET: Two Midtown Plaza, Suite 1400
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Microsoft Windows 95
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,208
; FILING DATE: 27-DEC-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/539944
; FILING DATE: 06-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colton, Laurence P.
; REGISTRATION NUMBER: 33371
; REFERENCE/DOCKET NUMBER: 10733-191B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 875-3555
; TELEFAX: (404) 875-8505
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: no
US-08-777-208-6

Query Match 100.0%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPL 4
|||
Db 1 AAPL 4

RESULT 6

US-08-693-653-1

; Sequence 1, Application US/08693653
; Patent No. 5780439
; GENERAL INFORMATION:
; APPLICANT: Mendy, Francois
; APPLICANT: Kahn, Jean-Maurice
; APPLICANT: Roger, Loic
; TITLE OF INVENTION: Improvements in or relating to organic
; TITLE OF INVENTION: compounds
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sandoz Corporation
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: NJ07936
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,653
; FILING DATE: 09-AUG-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/353,652
; FILING DATE:
; APPLICATION NUMBER: US 07/960,143
; FILING DATE: 13-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Battle, Carl
; REGISTRATION NUMBER: 30,731
; REFERENCE/DOCKET NUMBER: 510-5747
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 503-8532
; TELEFAX: (201) 503-8807
; TELEX: 240867
; INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
;   LENGTH: 4 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
;   ORGANISM: Synthetic
; FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: 1
;   OTHER INFORMATION: /label= 1a
;   OTHER INFORMATION: /note= "glutaryl derivative"
; FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: 4
;   OTHER INFORMATION: /label= 1b
;   OTHER INFORMATION: /note= "-p-nitro-anilide derivative"
US-08-693-653-1

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Query Match          100.0%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 AAPL 4
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Db      1 AAPL 4

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RESULT 7

US-08-698-575E-1

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; Sequence 1, Application US/08698575E
; Patent No. 5874585
; GENERAL INFORMATION:
;   APPLICANT:
;   TITLE OF INVENTION: SUBSTITUTED HETEROCYCLIC COMPOUNDS USEFUL AS
;   TITLE OF INVENTION: INHIBITORS OF (SERINE PROTEASES) HUMAN NEUTROPHIL
ELASTASE
;   NUMBER OF SEQUENCES: 4
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/698,575E
;   FILING DATE:
;   CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/345,820
;   FILING DATE:
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 4 amino acids
;   TYPE: amino acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-698-575E-1

Query Match 100.0%; Score 4; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
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Db 1 AAPL 4

RESULT 8

US-08-907-840A-3

; Sequence 3, Application US/08907840A
; Patent No. 5952307

; GENERAL INFORMATION:

; APPLICANT: Powers, James C.
; TITLE OF INVENTION: Basic Alpha-Aminoalkylphosphonate
; TITLE OF INVENTION: Derivatives
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Deveau, Colton & Marquis
; STREET: Two Midtown Plaza, Suite 1400
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Microsoft Windows 95
; SOFTWARE: Microsoft Word

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/907,840A
; FILING DATE: 14 AUG-1997
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/184286
; FILING DATE: 21 JAN-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Colton, Laurence P.
; REGISTRATION NUMBER: 33371
; REFERENCE/DOCKET NUMBER: 10733-175CIP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (404) 875-3555
; TELEFAX: (404) 875-8505

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: no

US-08-907-840A-3

Query Match 100.0%; Score 4; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
 ||||
Db 1 AAPL 4

RESULT 9

US-08-765-165-1
; Sequence 1, Application US/08765165
; Patent No. 5985273
; GENERAL INFORMATION:
; APPLICANT: Reed, Benjamin J.
; APPLICANT: Sandeman, Richard M.
; APPLICANT: Chandler, David S.
; TITLE OF INVENTION: BIOLOGICAL CONTROL OF INSECTS
; FILE REFERENCE: 08820/002001
; CURRENT APPLICATION NUMBER: US/08/765,165
; CURRENT FILING DATE: 1997-06-27
; EARLIER APPLICATION NUMBER: PCT/AU95/00347
; EARLIER FILING DATE: 1995-06-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic substrates
US-08-765-165-1

Query Match 100.0%; Score 4; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
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Db 1 AAPL 4

RESULT 10

US-09-069-823-1
; Sequence 1, Application US/09069823
; Patent No. 6037325
; GENERAL INFORMATION:
; APPLICANT: Gyorkos, Albert C.
; APPLICANT: Spruce, Lyle W.
; TITLE OF INVENTION: SUBSTITUTED HETEROCYCLIC COMPOUNDS
; TITLE OF INVENTION: USEFUL AS INHIBITORS OF (SERINE PROTEASES) HUMAN
NEUTROPHIL
; TITLE OF INVENTION: ELASTASE
; FILE REFERENCE: 20774.240087
; CURRENT APPLICATION NUMBER: US/09/069,823
; CURRENT FILING DATE: 1998-04-30

; EARLIER APPLICATION NUMBER: 08/345,820
; EARLIER FILING DATE: 1994-11-21
; EARLIER APPLICATION NUMBER: 08/698,575
; EARLIER FILING DATE: 1996-08-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Tetrapeptide
US-09-069-823-1

Query Match 100.0%; Score 4; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPL 4
|||
Db 1 AAPL 4

RESULT 11

US-09-578-303-10

; Sequence 10, Application US/09578303
; Patent No. 6399759
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Whitworth, S. Troy
; APPLICANT: Blum, Murray S.
; TITLE OF INVENTION: Ant Proteases and Methods of Inhibition
; FILE REFERENCE: 235.00150101
; CURRENT APPLICATION NUMBER: US/09/578,303
; CURRENT FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/136,331
; PRIOR FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: para-nitroanalide substrate
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: succinyl end cap
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: para-nitroanalide end cap
US-09-578-303-10

Query Match 100.0%; Score 4; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
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Db 1 AAPL 4

RESULT 12

US-08-988-842-3

; Sequence 3, Application US/08988842
; Patent No. 6462173
; GENERAL INFORMATION:
; APPLICANT: Lu, Jun Ping
; APPLICANT: Cantley, Lewis C.
; APPLICANT: Yaffe, Michael
; APPLICANT: Fischer, Gunter
; TITLE OF INVENTION: INHIBITORS OF PHOSPHOSERINE AND
; TITLE OF INVENTION: PHOSPHOTHREONINE-PROLINE-SPECIFIC ISOMERASES
; FILE REFERENCE: BIDMC97-02pA
; CURRENT APPLICATION NUMBER: US/08/988,842
; CURRENT FILING DATE: 1997-12-11
; EARLIER APPLICATION NUMBER: 60/058,164
; EARLIER FILING DATE:
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: synthetic nucleotide
; FEATURE:
; NAME/KEY: PHOSPHORYLATION
; LOCATION: (5)...(5)
US-08-988-842-3

Query Match 100.0%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
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Db 1 AAPL 4

RESULT 13

US-07-943-848-1

; Sequence 1, Application US/07943848
; Patent No. 5322839
; GENERAL INFORMATION:
; APPLICANT: Voegeli, Rainer
; APPLICANT: Stocker, Kurt
; APPLICANT: Mueller, Christian
; TITLE OF INVENTION: Protein Fraction For Cosmetic and
; TITLE OF INVENTION: Dermatologic Care of the Skin
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York


```

; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/943,848
; FILING DATE: 19920911
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Miller, Charles E.
; REGISTRATION NUMBER: 24,576
; REFERENCE/DOCKET NUMBER: 3006-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= No. 5322839e
; OTHER INFORMATION: /note= "Residue 1 has an amide terminal methoxy
; OTHER INFORMATION: succinyl group (MeOSuc)"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /label= No. 5322839e
; OTHER INFORMATION: /note= "Residue 4 has a carboxy terminal
; OTHER INFORMATION: para-nitroaniline group (pNA)"
US-07-943-848-1

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Query Match          75.0%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 AAP 3
        |||
Db      1 AAP 3

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RESULT 14
US-07-973-335-1
; Sequence 1, Application US/07973335
; Patent No. 5338547
; GENERAL INFORMATION:
; APPLICANT: Kennedy and Szuhaj
; TITLE OF INVENTION: No. 5338547el Bowman-Birk Inhibitor

```

```

; TITLE OF INVENTION: Product For Use As An Anticarcinogenesis Agent
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & No. 5338547ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/973,335
; FILING DATE: 19921102
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 824,719
; FILING DATE: January 17, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 579,155
; FILING DATE: September 6, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: UPSC-0003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-973-335-1

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Query Match          75.0%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches    3; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

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Qy      1 AAP 3
        |||
Db      1 AAP 3

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RESULT 15
US-08-155-331-18
; Sequence 18, Application US/08155331
; Patent No. 5441931
; GENERAL INFORMATION:
; APPLICANT: Foster, Donald C
; APPLICANT: Sprecher, Cindy
; APPLICANT: No. 5441931ris, Kjeld
; TITLE OF INVENTION: NOVEL HUMAN AMYLOID PROTEIN PRECURSOR

```

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; TITLE OF INVENTION:  HOMOLOG AND KUNITZ-TYPE INHIBITOR
; NUMBER OF SEQUENCES:  19
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  ZymoGenetics, Inc.
;   STREET:  4225 Roosevelt Way, N.E.
;   CITY:  Seattle
;   STATE:  WA
;   COUNTRY:  USA
;   ZIP:  98105
; COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/155,331
;   FILING DATE:
;   CLASSIFICATION:  435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/985,692
;   FILING DATE:  02-DEC-1992
; ATTORNEY/AGENT INFORMATION:
;   NAME:  Parker, Gary E
;   REGISTRATION NUMBER:  31-684
;   REFERENCE/DOCKET NUMBER:  92-21C1
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  206-547-8080 ext 322
;   TELEFAX:  206-548-2329
; INFORMATION FOR SEQ ID NO:  18:
; SEQUENCE CHARACTERISTICS:
;   LENGTH:  4 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  linear
; MOLECULE TYPE:  peptide
; FRAGMENT TYPE:  internal
; FEATURE:
;   NAME/KEY:  Modified-site
;   LOCATION:  1..4
;   OTHER INFORMATION:  /label= Ala-1
;   OTHER INFORMATION:  /note= "Amino-terminal alanine residue is capped
;   OTHER INFORMATION:  with a methoxysuccinyl gr..."
; FEATURE:
;   NAME/KEY:  Modified-site
;   LOCATION:  1..4
;   OTHER INFORMATION:  /label= Val-4
;   OTHER INFORMATION:  /note= "Carboxyl-terminal valine residue is capped
;   OTHER INFORMATION:  with p-nitroznilide"
US-08-155-331-18

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Query Match          75.0%;  Score 3;  DB 1;  Length 4;
Best Local Similarity 100.0%;  Pred. No. 2.5e+05;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

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Qy      1 AAP 3
        |||
Db      1 AAP 3

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Job time : 10.5714 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 12:16:11 ; Search time 28.5714 Seconds
(without alignments)
22.222 Million cell updates/sec

Title: US-10-033-526-3
Perfect score: 4
Sequence: 1 AAPL 4

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 50015

Minimum DB seq length: 4

Maximum DB seq length: 6

Post-processing: Listing first 45 summaries

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- 13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
- 14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
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- 20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
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- 22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
- 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

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2	4	100.0	4	18	AAW52605	Serine protease-in	
3	4	100.0	4	18	AAW29410	Elastolytic protei	
4	4	100.0	4	18	AAW26080	Substrate #3 for s	
5	4	100.0	4	18	AAW12811	Synthetic substrat	
6	4	100.0	4	19	AAW51756	Substrate used to	
7	4	100.0	4	19	AAW37769	Amino acid sequenc	
8	4	100.0	4	19	AAW39105	Calf thymus immuno	
9	4	100.0	4	20	AAW31241	Alpha-aminoalkyl p	
10	4	100.0	4	21	AAB03091	Substrate peptide	
11	4	100.0	4	22	AAB97637	Alpha-ketoamide el	
12	4	100.0	4	22	AAB35964	Elastase cleavable	
13	4	100.0	4	23	ABB83982	Chymotrypsin subst	
14	4	100.0	4	23	ABB81160	Matrix metalloprot	
15	4	100.0	4	23	AAE25711	Synthetic para-nit	
16	4	100.0	4	23	AAO15231	Porphyromonas ging	
17	4	100.0	4	23	AAO18045	C-terminal truncat	
18	4	100.0	4	23	ABB83183	Synthetic peptide	
19	3	75.0	4	5	AAP40001	Lipopeptide protea	
20	3	75.0	4	5	AAP40002	Lipopeptide protea	
21	3	75.0	4	5	AAP40457	N-terminal polyhyd	
22	3	75.0	4	5	AAP40458	N-terminal polyhyd	
23	3	75.0	4	5	AAP40459	N-terminal polyhyd	
24	3	75.0	4	5	AAP40460	N-terminal polyhyd	
25	3	75.0	4	5	AAP40363	Sequence of inhibi	
26	3	75.0	4	5	AAP40365	Sequence of inhibi	
27	3	75.0	4	11	AAR04012	Peptidase substrat	
28	3	75.0	4	12	AAR10886	Peptide component	
29	3	75.0	4	12	AAR10887	Peptide component	
30	3	75.0	4	12	AAR11222	Ketone analogue pr	
31	3	75.0	4	12	AAR11223	Ketone analogue pr	
32	3	75.0	4	13	AAR22056	Chromogenic substr	
33	3	75.0	4	13	AAR26240	Alpha-keto peptide	
34	3	75.0	4	13	AAR26241	Alpha-keto peptide	
35	3	75.0	4	13	AAR26242	Peptide keto ester	
36	3	75.0	4	13	AAR29963	Elastase-inhibitin	
37	3	75.0	4	13	AAR29964	Cathepsin G inhibi	
38	3	75.0	4	14	AAR32369	Morpholino urea de	
39	3	75.0	4	14	AAR34258	Chromogenic peptid	
40	3	75.0	4	14	AAR38407	Elastase inhibitor	
41	3	75.0	4	14	AAR38410	Cathepsin G inhibi	
42	3	75.0	4	14	AAR44109	Aminonaphthalene p	
43	3	75.0	4	15	AAR52024	Bacillus alkali pr	
44	3	75.0	4	15	AAR47852	Calpain inhibitor.	
45	3	75.0	4	15	AAR45969	Serine protease in	

ALIGNMENTS

RESULT 1

AAR46220

ID AAR46220 standard; peptide; 4 AA.

XX

AC AAR46220;

XX

DT 04-AUG-1994 (first entry)

XX

DE Serine protease inhibitor tetrapeptide.

XX

KW Prevention; schistosomiasis; parasite; infection; prevention;

KW parasitic penetration; skin; cercariae; anti-penetrant.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "BG(peptide blocking gp.) attached"

FT Modified-site 4

FT /note= "PI(protease inhibitor), other than
chloromethyl ketone, attached"

XX

PN US5284829-A.

XX

PD 08-FEB-1994.

XX

PF 26-NOV-1991; 91US-0798565.

XX

PR 26-NOV-1991; 91US-0798565.

XX

PA (REGC) UNIV CALIFORNIA.

XX

PI Cohen FE, McKerrow JH;

XX

DR WPI; 1994-056364/07.

XX

PT Synthetic tetra:peptide(s) with an N-terminal blocking gp. and

PT C-terminal enzyme inhibitor - can be formulated into soaps and

PT sprays and used to prevent schistosomal skin penetration

XX

PS Disclosure; Page 7; 35pp; English.

XX

CC The sequence is that of a synthetic tetrapeptide serine protease

CC inhibitor which can be used to prevent schistosome parasite

CC infection. It may be used in a formulation as a soap, lotion,

CC cream, spray, etc. to stop parasitic penetration of the skin.

XX

SQ Sequence 4 AA;

Query Match 100.0%; Score 4; DB 15; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4

||||

Db 1 AAPL 4

RESULT 2

AAW52605

ID AAW52605 standard; peptide; 4 AA.

XX

AC AAW52605;

XX

DT 22-JUN-1998 (first entry)

XX

DE Serine protease-inhibiting peptide with C-terminal phosphonate residue.

XX

KW Selective; serine protease inhibitor; trypsin; elastase; chymotrypsin;
KW antiinflammatory; anticoagulant; antitumour; Schistosoma mansoni.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "MeO-Suc-Ala"

FT Modified-site 4

FT /note= "Leu(P)-(OPh)2; where Leu(P) represents a
FT leucine analogue in which the carboxyl group
FT -COOH has been replaced by a phosphonate group
FT -P(=O)(OH)(OH); and (OPh)2 indicates that the
FT phosphonate has been diphenyl esterified"

XX

PN US5686419-A.

XX

PD 11-NOV-1997.

XX

PF 21-JAN-1994; 94US-0184286.

XX

PR 21-JAN-1994; 94US-0184286.

XX

PA (GEOR-) GEORGIA TECH RES CORP.

XX

PI Boduszek B, Oleksyszyn J, Powers JC;

XX

DR WPI; 1997-558177/51.

XX

PT New peptidyl derivatives of alpha-aminoalkyl phosphonic acid
PT di:ester - are serine protease inhibitors, useful e.g. for reducing
PT blood coagulation, controlling tumour invasion or treating
PT inflammation

XX

PS Example 13; Column 22; 16pp; English.

XX

CC The patent discloses new peptidyl derivatives of diesters of alpha-
CC aminoalkylphosphonic acids having basic substituents, of formula
CC X-AA4-AA3-AA2-NH-CHR-P(=O)(OZ)(OZ1), in which: R = B-substituted
CC phenyl, B-substituted benzyl or B-substituted 1-6C alkyl; B = amidino,
CC guanidino, isothioureido or amino; Z and Z1 = 1-6C perfluoroalkyl or
CC optionally substituted phenyl; AA2 = an L- or D-amino acid residue;
CC AA3 = a single bond or an L- or D-amino acid residue; AA4 = a single
CC bond or an L- or D-amino acid residue; X = H, NH2CO, NH2CS, NH2SO2,
CC YNHCO, YNHCS, YNHCO2, YCS, YSO2, YOCO, YOCS or YCO; Y = optionally
CC substituted 1-6C alkyl, 1-6C fluoroalkyl, 9-fluorenylmethyl, phenyl,

CC naphthyl, or 1-6C alkyl with 1-2, optionally substituted, attached
 CC phenyl groups. The new compounds are inhibitors of trypsin, elastase,
 CC chymotrypsin and other serine proteases; and their inhibitory activity
 CC is selective depending on the identity of the alpha-aminoalkylphosphonic
 CC acid ester residue. They can be used as antiinflammatory agents,
 CC anticoagulants and antitumour agents. The present sequence is
 CC an example of a compound which can specifically inhibit the activity
 CC of elastolytic proteinase from *Schistosoma mansoni*.

XX

SQ Sequence 4 AA;

Query Match 100.0%; Score 4; DB 18; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPL 4

||||

Db 1 AAPL 4

RESULT 3

AAW29410

ID AAW29410 standard; peptide; 4 AA.

XX

AC AAW29410;

XX

DT 25-MAR-2003 (updated)

DT 23-FEB-1998 (first entry)

XX

DE Elastolytic proteinase inhibitor peptide ketoamide derivative.

XX

KW Peptide ketoamide derivative; elastolytic proteinase inhibitor;

KW Alzheimer's disease; coagulation disorder; serine protease;

KW cysteine protease; calpain; cathepsin G; neurodegenerative disease;

KW ischaemia; stroke; trypsin inhibitor; chymase inhibitor; anticoagulant;

KW tissue damage; thrombosis; blistering; *Schistosoma mansoni*.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Succinyl-ala"

FT Modified-site 4

FT /note= "Leu-NR3R4, where R3 and R4 are selected

FT independently from the group consisting of H,

FT 1-20C alkyl, 3-20C cyclised alkyl, 1-20C

FT alkyl with a phenyl group (optionally mono-,

FT di- or tri-substituted with K) attached to the

FT 1-20C alkyl, 3-20C cyclised alkyl with an

FT attached phenyl group substituted with K, 1-20

FT alkyl with a morpholine, a pyrrolidine or a

FT piperidine ring attached through nitrogen to the

FT alkyl, 1-20C alkyl with an OH group attached to

FT the alkyl, 1-10C with an attached pyridyl

FT group or cyclohexyl group, -NHCH2CH2-

FT (4-hydroxyphenyl)- and -NHCH2CH2-(3-indolyl)"

XX

PN US5610297-A.
 XX
 PD 11-MAR-1997.
 XX
 PF 06-OCT-1995; 95US-0539946.
 XX
 PR 27-DEC-1991; 91US-0815073.
 PR 09-SEP-1993; 93US-0118997.
 PR 20-MAY-1994; 94US-0247081.
 XX
 PA (GEOR-) GEORGIA TECH RES CORP.
 XX
 PI Powers JC;
 XX
 DR WPI; 1997-178454/16.
 XX
 PT New peptide keto:amide derivs - are protease inhibitors used to
 PT treat e.g. Alzheimer's disease, coagulation disorders and other
 PT neurodegenerative disorders.
 XX
 PS Disclosure; Columns 17-18; 17pp; English.
 XX
 CC The present sequence represents a peptide ketoamide derivative which is
 CC useful for selectively inhibiting elastolytic proteinase from
 CC Schistosoma mansoni. It is a specific example of a new class of peptides
 CC which selectively inhibit serine proteases or cysteine proteases,
 CC including calpains and cathepsin B. The calpain inhibitors are useful for
 CC treatment of various neurodegenerative diseases and conditions including
 CC ischaemia, stroke and Alzheimer's disease. The protease inhibitors,
 CC especially the elastase, trypsin and chymase inhibitors, are used to
 CC control tissue damage and various inflammatory conditions mediated by
 CC proteases, such as blistering. They are also useful as anticoagulants and
 CC can be used to treat thrombosis. The peptides may also be used to
 CC identify new proteolytic enzymes encountered in research. Further, they
 CC may also be useful in research and industrially to prevent undesired
 CC proteolysis that occurs during the production, isolation, purification,
 CC transport and storage of valuable peptides and proteins; e.g. they may be
 CC added to antibodies, enzymes, plasma proteins, tissue extracts or other
 CC proteins and peptides which are widely sold for use in clinical analyses,
 CC biomedical research and for many other reasons.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 4 AA;

Query Match 100.0%; Score 4; DB 18; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
 ||||
 Db 1 AAPL 4

RESULT 4
 AAW26080
 ID AAW26080 standard; peptide; 4 AA.
 XX

AC AAW26080;
 XX
 DT 25-MAR-2003 (updated)
 DT 05-NOV-1997 (first entry)
 XX
 DE Substrate #3 for serine protease.
 XX
 KW Serine protease; substrate; Streptomyces griseus; guanidine; pre-soak;
 KW cleaning composition; laundry detergent; additive composition; enzyme;
 KW dishwasher detergent; drain opener; urea; contact lens cleanser;
 KW proteinaceous stain.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "succinylated"
 FT Modified-site 4
 FT /note= "para-nitroanilidated"
 XX
 PN US5646028-A.
 XX
 PD 08-JUL-1997.
 XX
 PF 17-OCT-1995; 95US-0544143.
 XX
 PR 18-JUN-1991; 91US-0718303.
 PR 06-NOV-1992; 92US-0973343.
 PR 18-AUG-1994; 94US-0292924.
 PR 17-OCT-1995; 95US-0544143.
 XX
 PA (CLRXX) CLOROX CO.
 XX
 PI Leigh SD;
 XX
 DR WPI; 1997-362936/33.
 XX
 PT Serine protease from Streptomyces griseus ATCC 55178 - with good
 PT stability in presence of urea or guanidine, useful in cleaning
 PT compositions, including laundry and dishwashing detergents
 XX
 PS Example 1; Column 12; 16pp; English.
 XX
 CC AAW26078-W26096 represent substrates for the serine protease of the
 CC invention. The serine protease recognises these sequences, but is
 CC specific for the sequence shown in AAW24567. The protease has the
 CC N-terminal and C-terminal sequences represented by AAW24565 and AAW24566
 CC respectively. The serine protease was isolated from Streptomyces griseus
 CC variety alkaliphilus No. 33 (ATCC 55178). The protease has an apparent
 CC molecular weight of 19 kD (by reducing sodium dodecylsulphate
 CC polyacrylamide gel electrophoresis), and improved stability against urea
 CC and guanidine. The protease is inhibited by phenylmethylsulphonyl
 CC fluoride. The serine protease is useful in liquid or granular cleaning
 CC compositions, specifically laundry detergents or additive compositions.
 CC It is also useful in automatic dishwasher detergents, pre-soaks, drain
 CC openers, contact lens cleansers etc. The protease has better activity
 CC against proteinaceous stains than known enzymes and unusually high

CC stability in the presence of chaotropic agents.

CC (Updated on 25-MAR-2003 to correct PF field.)

XX

SQ Sequence 4 AA;

Query Match 100.0%; Score 4; DB 18; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4

||||

Db 1 AAPL 4

RESULT 5

AAW12811

ID AAW12811 standard; peptide; 4 AA.

XX

AC AAW12811;

XX

DT 21-APR-1997 (first entry)

XX

DE Synthetic substrate #2 for cold-adapted alkali protease.

XX

KW Cold-adapted alkali protease; alteromonas; urea-denatured haemoglobin;

KW yolk; casein; p-nitroaniline; detergent; meat softener.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /label= Succinylated

FT Modified-site 4

FT /label= p-nitroanilinylation

XX

PN JP08322562-A.

XX

PD 10-DEC-1996.

XX

PF 01-JUN-1995; 95JP-0135056.

XX

PR 01-JUN-1995; 95JP-0135056.

XX

PA (KAOS) KAO CORP.

XX

DR WPI; 1997-081078/08.

XX

PT Cold-adapted alkali protease - produced by Alteromonas, used in

PT detergents

XX

PS Claim 1; Page 2; 10pp; Japanese.

XX

CC AAW12810-W12812 represent synthetic substrates for the cold-adapted

CC alkali protease of the invention. The alkali protease of the invention

CC is produced by Alteromonas, specifically by Alteromonas species KSM-SP

CC 111 which is isolated from a shellfish in the Antarctic ocean. The

CC enzyme of the invention has an active temperature of 0-70 degrees C, with

CC an optimum of 40 degrees, and with 20% of activity retained at 10
 CC degrees, and 10% maintained at 0 degrees. The pH range of the enzyme is
 CC 4-14, with an optimum of 11, but 70% (or higher) of the activity
 CC maintained at pH12. The protease has a molecular weight of 54000, as
 CC determined by SDS-polyacrylamide gel electrophoresis. The enzyme is
 CC capable of acting on casein, urea-denatured haemoglobin, yolk, and the
 CC synthetic substrates represented by these sequences, to yield
 CC p-nitroaniline. The enzyme is inhibited by the Hg and Zn metal ions,
 CC EDTA, phenylmethanesulphonyl fluoride, chymostatin or
 CC p-chloromercuribenzoic acid. Activity of the enzyme is increased 2-7
 CC times by the presence of sodium alkanesulphate, sodium
 CC alpha-olefinesulphate, sodium polyoxyethylenealkylsulphate, softanol 70H
 CC or alpha-sulphofatty acid ester. The protease can be used as a component
 CC of detergents, or as a softener for meat when used at a lower
 CC temperature.
 XX
 SQ Sequence 4 AA;

Query Match 100.0%; Score 4; DB 18; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
 ||||
 Db 1 AAPL 4

RESULT 6

AAW51756

ID AAW51756 standard; peptide; 4 AA.

XX

AC AAW51756;

XX

DT 10-SEP-1998 (first entry)

XX

DE Substrate used to assay rotamase activity of 50-54 kDa immunophilin.

XX

KW immunophilin; tryptic peptide; C-terminus; FK-506; cyclosporine A;

KW rapamycin; immunosuppressant drug; binding assay.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Succinyl-Ala"

FT Modified-site 4

FT /note= "Leu-para-nitroanilide"

XX

PN US5780307-A.

XX

PD 14-JUL-1998.

XX

PF 26-JUL-1996; 96US-0686759.

XX

PR 23-FEB-1994; 94US-0200404.

PR 02-DEC-1988; 88US-0279176.

PR 02-MAR-1990; 90US-0487115.

PR 09-MAY-1990; 90US-0521074.
 PR 22-OCT-1991; 91US-0782761.
 PR 26-FEB-1992; 92US-0841792.
 PR 26-JUL-1996; 96US-0686759.
 XX
 PA (SOLD/) SOLDIN S J.
 XX
 PI Soldin SJ;
 XX
 DR WPI; 1998-413070/35.
 XX
 PT New immunophilin from mammalian lymphoid tissue - used in binding
 PT assays for cyclosporine, FK-506 and rapamycin, and for recovering new
 PT immunosuppressants from extracts and cell cultures
 XX
 PS Example 18; Columns 31-32; 56pp; English.
 XX
 CC The invention relates to an immunophilin (i.e. a cytosolic immuno-
 CC suppressant drug binding protein) that binds specifically to FK-506,
 CC cyclosporine A and rapamycin; has molecular weight 34-47 kD (by
 CC chromatography, sodium dodecylsulphate-polyacrylamide gel
 CC electrophoresis or amino acid analysis) and has isoelectric point (pI)
 CC 6.5-7. It is optionally immobilised on a solid support, is used in
 CC binding assays for the specified immunosuppressants, and for capturing
 CC potential immunosuppressants from microbial extracts or cell cultures,
 CC e.g. active metabolites of the specified immunosuppressants or their
 CC mammalian homologues. The present sequence represents a peptide
 CC substrate which was used to assay the rotamase activity of a 50-54 kDa
 CC immunophilin.
 XX
 SQ Sequence 4 AA;

 Query Match 100.0%; Score 4; DB 19; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 AAPL 4
 ||||
 Db 1 AAPL 4

RESULT 7

AAW37769

ID AAW37769 standard; Protein; 4 AA.
 XX
 AC AAW37769;
 XX
 DT 20-JUL-1998 (first entry)
 XX
 DE Amino acid sequence of synthetic chromogenic substrate.
 XX
 KW Subtilisin-type serine protease inhibitor; inhibition; ss;
 KW proteolytic activity; extracellular elastolytic serine protease;
 KW Aspergillus hyphae; lung; germination; aspergillosis; nasal delivery;
 KW chromogenic substrate.
 XX
 OS Synthetic.

```

XX
FH      Key      Location/Qualifiers
FT      Active-site
FT      Modified-site 1
FT      /note= "Suc-Ala"
FT      Modified-site 4
FT      /note= "Leu-pNa"
XX
PN      US5739283-A.
XX
PD      14-APR-1998.
XX
PF      07-JUN-1995; 95US-0486895.
XX
PR      07-JUN-1995; 95US-0486895.
XX
PA      (OHIO-) OHIO STATE RES FOUND.
XX
PI      Ceselski SK, Copelan EA, Kolattukudy PE, Markaryan AN;
XX
DR      WPI; 1998-250492/22.
XX
PT      Treatment of invasive pulmonary aspergillosis - by nasal
PT      administration of composition comprising subtilisin type serine
PT      protease inhibitor e.g. streptomyces subtilisin inhibitor, and
PT      carrier e.g. phosphate buffered saline
XX
PS      Claim 6; Columns 17-18; 12pp; English.
XX
CC      The amino acid sequence is a chromogenic substrate used in the
CC      method of invention to develop subtilisin-type serine protease
CC      inhibitor (SSI). The SSI inhibits the proteolytic activity of the
CC      extracellular elastolytic serine protease produced by aspergillus and
CC      reduces the invasion of the lung and tissues surrounding it by the
CC      germinating hyphae of aspergillus. It can be used in a drug
CC      composition to treat aspergillosis via nasal delivery.
XX
SQ      Sequence 4 AA;

Query Match      100.0%; Score 4; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAPL 4
        ||||
Db      1 AAPL 4

```

```

RESULT 8
AAW39105
ID      AAW39105 standard; peptide; 4 AA.
XX
AC      AAW39105;
XX
DT      08-APR-1998 (first entry)
XX
DE      Calf thymus immunophilin rotamase substrate 6.

```

```

XX
KW  Immunophilin; calf; immunosuppressant drug; FK506; rapamycin;
KW  cyclosporin A; rotamase; therapy.
XX
OS  Synthetic.
XX
FH  Key          Location/Qualifiers
FT  Modified-site 1
FT                      /note= "N-terminal Suc-Ala"
FT  Modified-site 4
FT                      /note= "C-terminal Leu-pNA"
XX
PN  US5698448-A.
XX
PD  16-DEC-1997.
XX
PF  08-APR-1994; 94US-0224868.
XX
PR  23-FEB-1994; 94US-0200404.
PR  02-DEC-1988; 88US-0279176.
PR  02-MAR-1990; 90US-0487115.
PR  09-MAY-1990; 90US-0521074.
PR  22-OCT-1991; 91US-0782761.
PR  26-FEB-1992; 92US-0841792.
PR  08-APR-1994; 94US-0224868.
XX
PA  (SOLD/) SOLDIN S J.
XX
PI  Soldin SJ;
XX
DR  WPI; 1998-051496/05.
XX
PT  Immunophilin protein that binds immunosuppressant drugs - useful in
PT  assays for cyclosporin A, FK506 and rapamycin
XX
PS  Example 18; Column 31; 54pp; English.
XX
CC  Peptides AAW39100-W39110 represent substrates used in an assay to
CC  investigate the rotamase activity of a 10-12 kDa and a 50-52 kDa
CC  immunophilin isolated from calf thymus. Immunophilins are proteins
CC  capable of binding to immunosuppressant drugs, in this example FK506,
CC  rapamycin or cyclosporin. This substrate has a rotamase activity of
CC  0.45 K-obs (min-1) with the 50-52 kDa immunophilin and 0.93 K-obs
CC  (min-1) with the 10-12 kDa immunophilin. Immunophilins will have
CC  applications for monitoring immunosuppressive therapy and for the capture
CC  of potential immunosuppressive drugs from microbial extract, culture
CC  media or from mammalian body fluids and tissues.
XX
SQ  Sequence 4 AA;

Query Match          100.0%; Score 4; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAPL 4
        ||||
Db      1 AAPL 4

```


RESULT 9

AAAY31241

ID AAY31241 standard; peptide; 4 AA.

XX

AC AAY31241;

XX

DT 09-NOV-1999 (first entry)

XX

DE Alpha-aminoalkyl phosphonate derivative peptide 3.

XX

KW Alpha-aminoalkyl phosphonate; serine protease inhibitor; anticoagulant;
 KW cytostatic; anti-inflammatory; gastrointestinal; endocrine; respiratory;
 KW dermatological; chymotrypsin inhibitor; elastase inhibitor; inflammation;
 KW tryptase inhibitor; trypsin inhibitor; blood coagulation; pancreatitis;
 KW tumour invasion control; emphysema; respiratory distress syndrome;
 KW skin blistering.

XX

OS Synthetic.

XX

PN US5952307-A.

XX

PD 14-SEP-1999.

XX

PF 14-AUG-1997; 97US-0907840.

XX

PR 14-AUG-1997; 97US-0907840.

PR 21-JAN-1994; 94US-0184286.

XX

PA (GEOR-) GEORGIA TECH RES CORP.

XX

PI Jackson DS, Ni L, Powers JC;

XX

DR WPI; 1999-539191/45.

XX

PT New aminoalkyl phosphonate derivatives are serine protease
 PT inhibitors useful for decreasing blood coagulation and for treating
 PT tumour invasion, inflammation, pancreatitis, emphysema, respiratory
 PT distress syndrome and skin blistering

XX

PS Disclosure; Column 31-32; 18pp; English.

XX

CC This invention describes the production of novel alpha-aminoalkyl
 CC phosphonate derivatives (I) which have anticoagulant, cytostatic,
 CC anti-inflammatory, gastrointestinal, endocrine, respiratory and
 CC dermatological activity. The products of the invention are also found
 CC to act as serine protease inhibitors, chymotrypsin inhibitors, elastase
 CC inhibitors, tryptase inhibitors and trypsin inhibitors. (I) are useful
 CC for decreasing blood coagulation, and for controlling tumour invasion,
 CC inflammations, pancreatitis, emphysema, respiratory distress syndrome
 CC and skin blistering. AAY31239-Y31241 are peptides used to describe the
 CC method of the invention.

XX

SQ Sequence 4 AA;

Query Match

100.0%; Score 4; DB 20; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
 ||||
Db 1 AAPL 4

RESULT 10

AAB03091

ID AAB03091 standard; peptide; 4 AA.

XX

AC AAB03091;

XX

DT 10-OCT-2000 (first entry)

XX

DE Substrate peptide #2.

XX

KW Serine protease; trypsin activity; Trichoderma; bacterial; coagulant;
KW hypertensive; antiinflammatory; leather preparation; silk treatment.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Conjugated to succinyl moiety"

FT Modified-site 4

FT /note= "Conjugated to p-nitroaniline (pNA)"

XX

PN JP2000116377-A.

XX

PD 25-APR-2000.

XX

PF 08-OCT-1998; 98JP-0303263.

XX

PR 08-OCT-1998; 98JP-0303263.

XX

PA (AMAN) AMANO PHARM KK.

XX

DR WPI; 2000-369402/32.

XX

PT A new serine protease and its preparation, used clinically in blood
PT coagulation, hypotension and anti-inflammation -

XX

PS Example 3; Page 5; 9pp; Japanese.

XX

CC The invention relates to a novel serine protease from Trichoderma sp.

CC No.9064. The N-terminus of this protease is given in AAB03085. The novel
CC protease has trypsin-like activity, specifically cleaving peptide chains
CC on the carboxyl side of a basic amino acid (e.g., arginine or lysine).

CC It has a pH optimum of 7-8, and is stable between pH 5 and pH10. It has
CC a temperature optimum of approximately 40 degrees Celsius, and is stable
CC between 40 and 50 degrees Celsius. The invention also relates to a

CC method for the preparation of the novel serine protease, and the use of
CC the protease in protein degradation. The enzyme has coagulant,

CC hypertensive and anti-inflammatory effects. It may also be used in the
CC preparation of leather, for raw silk treatment and for the preparation of

CC protein hydrolysate. Sequences AAB03090-B03094 represent tetrapeptides
CC used in the determination of the activity of the novel protease.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 4; DB 21; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
|||
Db 1 AAPL 4

RESULT 11

AAB97637

ID AAB97637 standard; peptide; 4 AA.

XX

AC AAB97637;

XX

DT 21-SEP-2001 (first entry)

XX

DE Alpha-ketoamide elastolytic proteinase inhibitor peptide.

XX

KW Peptide ketoamide; serine protease inhibitor;
KW cysteine protease inhibitor; transition state analogue;
KW neurodegenerative disease; ischaemia; stroke; Alzheimer's disease;
KW anticoagulant; thrombosis; adult respiratory distress syndrome;
KW emphysema; rheumatoid arthritis; pancreatitis; viral infection;
KW muscular dystrophy; myocardial tissue damage; tumour metastasis;
KW bone resorption; Schistosoma mansoni; elastolytic protease inhibitor.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Suc-Ala"

FT Modified-site 4

FT /note= "Leu-CO-NR3R4"

XX

PN US6235929-B1.

XX

PD 22-MAY-2001.

XX

PF 27-DEC-1996; 96US-0777354.

XX

PR 27-DEC-1991; 91US-0815073.

PR 09-SEP-1993; 93US-0118997.

PR 20-MAY-1994; 94US-0246511.

PR 06-OCT-1995; 95US-0539944.

XX

PA (GEOR-) GEORGIA TECH RES CORP.

XX

PI Powers JC;

XX

DR WPI; 2001-440210/47.

XX

PT New tripeptide ketoamide derivatives are serine and cysteine protease
PT inhibitors, useful as anticoagulants and for treating neurodegenerative
PT diseases, thrombosis, emphysema and rheumatoid arthritis -
XX
PS Disclosure; Column 18; 24pp; English.
XX
CC The invention relates to peptide ketoamide derivatives useful for
CC selectively inhibiting serine proteases and cysteine proteases, and for
CC generally inhibiting all members of these classes of enzymes. The peptide
CC ketoamides are derivatives of substrate peptides of serine and cysteine
CC proteases and act as transition state analogues. The peptides of the
CC invention have the formula M1-AA1-AA2-AA3-CO-NR3R4 where:
CC M1 is NH2CO-, NH2CS-, NH2SO2-, XNHCO-, X2NCO-, XNHCS-, X2NCS-,
CC XNHSO2-, X2NSO2-, XCO-, XCS-, XSO2-, XOCO- or XOCS;
CC X is 1-10C (fluoro)alkyl (optionally substituted by J), 1-adamantyl,
CC 9-fluorenyl, phenyl or naphthyl (optionally substituted by up to 3 of
CC K), or 1-10C alkylphenyl, 1-10C alkylidiphenyl or 1-10C alkylphenoxy
CC (all optionally substituted by K);
CC J is halo, COOH, OH, CN, NO2, NH2, 1-10C alkoxy, 1-10C alkylamine,
CC 2-12C dialkylamine, 1-10C alkyl-OCO-, 1-10C alkyl-OCONH- or 1-10C
CC alkylthio;
CC K is halo, 1-10C (perfluoro)alkyl, 1-10C alkoxy, NO₂, CN, OH, COOH,
CC NH2, 1-10C alkylamino, 2-12C dialkylamino, 1-10C acyl, 1-10C alkoxy-CO
CC or 1-10C alkylthio;
CC AA1, AA2 are independently Ala, Val, Leu, Ile, Gly, Ser, Asp or Glu;
CC AA3 is Asp or Glu, in either the L or D form;
CC R3 is 2-3C alkylphenyl, 3-20C cycloalkylphenyl, 1-20C alkylphenyl
CC (substituted by up to 3 of K), 3-20C cycloalkylphenyl (substituted by
CC K), NH-CH2CH2-(4-hydroxyphenyl) or NH-CH2CH2-(3-indolyl); and
CC R4 = H, 3-20C alkyl, cycloalkyl, 1-20C alkylphenyl (optionally
CC substituted by up to 3 of K), 3-20C cycloalkylphenyl (optionally
CC substituted by K), NHCH2CH2-(4-hydroxyphenyl) or
CC NHCH2CH2-(3-indolyl).
CC The peptide ketoamides are useful for treating neurodegenerative diseases
CC (including ischaemia, stroke and Alzheimer's disease), as anticoagulants,
CC and for treating thrombosis. They are also useful for treating
CC emphysema, adult respiratory distress syndrome, rheumatoid arthritis,
CC pancreatitis, viral infections, muscular dystrophy, myocardial tissue
CC damage, tumour metastasis and bone resorption. The present sequence
CC represents a Schistosoma mansoni elastolytic protease peptide
CC inhibitor.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 4; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPL 4
| | | |
Db 1 AAPL 4

RESULT 12
AAB35964
ID AAB35964 standard; peptide; 4 AA.
XX

AC AAB35964;
 XX
 DT 01-MAR-2001 (first entry)
 XX
 DE Elastase cleavable peptide #2.
 XX
 KW Polymeric drug conjugate; enzymatically cleavable linker; cardiant;
 KW antiinflammatory; cytostatic; hepatotropic; neuroprotective; cancer;
 KW antibacterial; nephrotropic; immunomodulatory; neoplastic disease;
 KW chronic inflammatory disease; acute inflammatory disease;
 KW cardiac disease; renal disease; liver disease; lung disease;
 KW neurological disease; musculoskeletal disease; immunological disorder;
 KW microbial infection.
 XX
 OS Synthetic.
 XX
 PN WO200064486-A2.
 XX
 PD 02-NOV-2000.
 XX
 PF 28-APR-2000; 2000WO-US11670.
 XX
 PR 28-APR-1999; 99US-0131404.
 PR 02-NOV-1999; 99US-0163090.
 XX
 PA (VERI-) VERITAS MEDICAL TECHNOLOGIES INC.
 XX
 PI Pachence JM, Belinka BA, Ramani T;
 XX
 DR WPI; 2001-031659/04.
 XX
 PT Polymeric drug conjugate, for treating diseases associated with organs
 PT e.g. liver or heart, has biologically active agents linked to regular
 PT repeating linear or branched co-polymers by enzymatically cleavable
 PT marker -
 XX
 PS Claim 30; Page 93; 100pp; English.
 XX
 CC This invention relates to a polymeric drug conjugate. The drug conjugate
 CC comprises biologically active agents conjugated via an enzymatically
 CC cleavable linker to a regular repeating linear unit comprising a water
 CC soluble polymer segment and a multifunctional chemical moiety, or to a
 CC branched polymer comprising two or more water soluble polymer segments
 CC each bound to a common multifunctional chemical moiety. The polymeric
 CC drug conjugate has antiinflammatory; cytostatic; cardiant; hepatotropic;
 CC neuroprotective; antibacterial; nephrotropic; and immunomodulatory
 CC activity. The drug conjugate is useful for alleviating a pathological
 CC condition such as neoplastic diseases, chronic inflammatory diseases
 CC acute inflammatory diseases, cardiac diseases, renal diseases, liver
 CC diseases, lung diseases, neurological diseases, musculoskeletal diseases
 CC and immunological disorders and various microbial infections by
 CC modulating immunological or hormonal function. The present sequence
 CC represents a peptide which can be used as the enzymatically cleavable
 CC linker in the drug conjugate of the invention.
 XX
 SQ Sequence 4 AA;

Query Match 100.0%; Score 4; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
|||
Db 1 AAPL 4

RESULT 13

ABB83982

ID ABB83982 standard; peptide; 4 AA.

XX

AC ABB83982;

XX

DT 13-DEC-2002 (first entry)

XX

DE Chymotrypsin substrate peptide 3.

XX

KW Chymotrypsin; protease; chymostatin; diisopropyl fluoro phosphate;
KW phenyl methane sulfonyl fluoride; angiotensin I; foodstuff.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "glutaryl group"

XX

PN JP2002125665-A.

XX

PD 08-MAY-2002.

XX

PF 27-OCT-2000; 2000JP-0329032.

XX

PR 27-OCT-2000; 2000JP-0329032.

XX

PA (AMAN) AMANO PHARM KK.

XX

DR WPI; 2002-709282/77.

XX

PT Novel chymotrypsin-like protease that has substrate specificity, that
PT hydrolyses human angiotensin I and synthetic substrates, and is
PT inhibited by serine protease inhibitor, useful for preparing foodstuffs

PT -

XX

PS Example 3; Page 5-6; 10pp; Japanese.

XX

CC The invention relates to a chymotrypsin-like protease that has substrate
CC specificity, hydrolyses human angiotensin I, has optimum pH of 8,
CC optimum temperature of 40oC, is stable at pH range of 5.0-11.5 and
CC temperature range of 40oC, has a molecular weight of 31000, has an
CC isoelectric point of 8.5 and is inhibited by chymostatin, diisopropyl
CC fluoro phosphate, phenyl methane sulfonyl fluoride and serine protease
CC inhibitor. The chymotrypsin-like protease has a high substrate
CC specificity and is useful for preparing foodstuffs and degrading
CC proteins. The present sequence is that of a peptide substrate of the
CC chymotrypsin-like protease, used in examples of the invention.

XX

SQ Sequence 4 AA;

Query Match 100.0%; Score 4; DB 23; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4

||||

Db 1 AAPL 4

RESULT 14

ABB81160

ID ABB81160 standard; peptide; 4 AA.

XX

AC ABB81160;

XX

DT 25-NOV-2002 (first entry)

XX

DE Matrix metalloproteinase peptide substrate #13.

XX

KW MMP; extracellular matrix; ECM; collagen; elastin; fibrin; ECM;
KW vulnerary; antiarthritic; osteopathic; antiinflammatory; nootropic;
KW ophthalmological; cytostatic; neuroprotective; antipsoriatic; elastase;
KW dermatological; vasotropic; antidiabetic; gynecological; antiulcer;
KW antirheumatic; matrix metalloproteinase; collagenase; stromelysin.

XX

OS Synthetic.

XX

PN WO200253172-A2.

XX

PD 11-JUL-2002.

XX

PF 21-DEC-2001; 2001WO-US49272.

XX

PR 29-DEC-2000; 2000US-0753078.

XX

PA (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX

PI McGrath KP, Quirk S;

XX

DR WPI; 2002-643296/69.

XX

PT Use of matrix metalloproteinase peptide substrate for the inhibition of
PT extracellular matrix degradation and for the treatment of wounds -

XX

PS Claim 29; Page 16; 46pp; English.

XX

CC The invention relates to the inhibition of extracellular matrix (ECM)
CC degradation or treatment of wounds involves administering at least one
CC substrate peptide (A) that competes with the ECM or natural proteins for
CC proteinaceous activity. The natural protein is collagen, elastin, fibrin
CC or other ECM proteins. The peptides act as matrix metalloproteinase
CC (MMP(s)) (collagenase, elastase, human neutrophil elastase, stromelysin)
CC antagonists. The peptide substrates are used for treating wounds,
CC particularly chronic wounds; and other diseases and disorders involving

CC uncontrolled breakdown of connective tissues by MMPs e.g. rheumatoid
 CC arthritis, osteoarthritis, osteopenias (osteoporosis, periodontitis,
 CC gingivitis, corneal epidermal and gastric ulceration), tumour metastasis,
 CC invasion and growth; neuroinflammatory disorders (including those
 CC involving myelin degradation e.g. multiple sclerosis), and angiogenesis
 CC dependant diseases (including angiofibromas, solid tumours, blood-borne
 CC tumours, leukemia, metastasis, telangiectasia, psoriasis, scleroderma,
 CC pyogenic granuloma, myocardial angiogenesis, plaque neovascularization,
 CC coronary collaterals, ischaemic limb angiogenesis, corneal diseases,
 CC rubeosis, neovascular glaucoma, diabetic retinopathy, retrolateral
 CC fibroplasia, diabetic neovascularization, macular degeneration, fracture,
 CC keloids, vasculogenesis, haematopoiesis, ovulation, menstruation and
 CC placentation). The peptides are further useful for in vitro application
 CC for regulation of MMPs in synthetic models to study wound healing.
 CC Sequences ABB81148-167 represent specific examples of the MMP peptide
 CC substrates of the invention.
 XX
 SQ Sequence 4 AA;

Query Match 100.0%; Score 4; DB 23; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
 ||||
 Db 1 AAPL 4

RESULT 15

AAE25711

ID AAE25711 standard; peptide; 4 AA.

XX

AC AAE25711;

XX

DT 04-NOV-2002 (first entry)

XX

DE Synthetic para-nitroanilide substrate #4.

XX

KW Chymotrypsin-like polypeptide; elastase-like polypeptide; amidolytic;

KW

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Linked to succinyl end cap"

FT Modified-site 4

FT /note= "Linked to para-nitroanilide end cap"

XX

PN US6399759-B1.

XX

PD 04-JUN-2002.

XX

PF 25-MAY-2000; 2000US-0578303.

XX

PR 27-MAY-1999; 99US-136331P.

XX

PA (UYGE-) UNIV GEORGIA RES FOUND INC.
 XX
 PI Travis J, Whitworth ST, Blum MS;
 XX
 DR WPI; 2002-546298/58.
 XX
 PT Novel isolated nucleic acid fragment encoding a serine protease, useful
 PT in identifying molecules that inhibit its activity, and in the
 PT development of insecticides to control fire ant infestation -
 XX
 PS Example 1; Column 19; 31pp; English.
 XX
 CC The invention relates to polypeptides including chymotrypsin-like
 CC polypeptides and elastase-like polypeptides, having amidolytic activity
 CC for cleavage of a peptide bond present in a target polypeptide. Nucleic
 CC acid encoding the polypeptides of the invention is useful to transform
 CC a host cell which optionally includes one or more marker sequences,
 CC which encodes a polypeptide that inactivates or detects a compound in
 CC the growth medium. The encoded polypeptide can be used to develop an
 CC inhibitor that reduces the amidolytic activity of the polypeptide,
 CC and the inhibitor can then be used to reduce the amount of solid food
 CC digested by a *Solenopsis invicta* 4th instar larva or colony. The
 CC present sequence is a synthetic para-nitroanilide substrate used in
 CC the exemplification of the invention.
 XX
 SQ Sequence 4 AA;

 Query Match 100.0%; Score 4; DB 23; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 AAPL 4
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 Db 1 AAPL 4

Search completed: December 30, 2003, 12:23:06
 Job time : 29.5714 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 12:23:47 ; Search time 20.2857 Seconds
 (without alignments)
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Title: US-10-033-526-3
 Perfect score: 4
 Sequence: 1 AAPL 4

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 724715 seqs, 199017464 residues

Word size : 0

Total number of hits satisfying chosen parameters: 18921

Minimum DB seq length: 4

Maximum DB seq length: 6

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4	100.0	4	10	US-09-935-744-2	Sequence 2, Appli
2	4	100.0	4	14	US-10-033-526-3	Sequence 3, Appli
3	4	100.0	5	15	US-10-206-699-143	Sequence 143, App
4	4	100.0	6	15	US-10-193-768-3	Sequence 3, Appli
5	3	75.0	4	9	US-09-842-543-1	Sequence 1, Appli
6	3	75.0	4	9	US-09-757-908A-14	Sequence 14, Appl
7	3	75.0	4	9	US-09-757-908A-15	Sequence 15, Appl
8	3	75.0	4	10	US-09-117-380B-1	Sequence 1, Appli
9	3	75.0	4	10	US-09-117-380B-2	Sequence 2, Appli
10	3	75.0	4	10	US-09-935-744-1	Sequence 1, Appli
11	3	75.0	4	11	US-09-928-117-1	Sequence 1, Appli
12	3	75.0	4	11	US-09-876-904A-19	Sequence 19, Appl
13	3	75.0	4	12	US-10-373-794-2	Sequence 2, Appli
14	3	75.0	4	12	US-10-373-794-3	Sequence 3, Appli
15	3	75.0	4	12	US-10-354-706-1	Sequence 1, Appli
16	3	75.0	4	12	US-10-350-470-10	Sequence 10, Appl
17	3	75.0	4	12	US-10-125-222-1	Sequence 1, Appli
18	3	75.0	4	12	US-10-137-867-76	Sequence 76, Appl
19	3	75.0	4	12	US-10-259-609-29	Sequence 29, Appl
20	3	75.0	4	12	US-10-352-786-63	Sequence 63, Appl
21	3	75.0	4	12	US-10-352-786-65	Sequence 65, Appl
22	3	75.0	4	14	US-10-090-624-33	Sequence 33, Appl
23	3	75.0	4	14	US-10-036-371-7	Sequence 7, Appli
24	3	75.0	4	14	US-10-040-655-10	Sequence 10, Appl
25	3	75.0	4	14	US-10-040-655-11	Sequence 11, Appl
26	3	75.0	4	14	US-10-154-507-6	Sequence 6, Appli
27	3	75.0	4	14	US-10-154-507-7	Sequence 7, Appli
28	3	75.0	4	14	US-10-154-507-13	Sequence 13, Appl
29	3	75.0	4	14	US-10-154-507-14	Sequence 14, Appl
30	3	75.0	4	14	US-10-154-507-15	Sequence 15, Appl
31	3	75.0	4	14	US-10-154-507-16	Sequence 16, Appl
32	3	75.0	4	14	US-10-033-526-1	Sequence 1, Appli
33	3	75.0	4	14	US-10-033-526-2	Sequence 2, Appli
34	3	75.0	4	14	US-10-041-006A-10	Sequence 10, Appl
35	3	75.0	4	14	US-10-041-006A-11	Sequence 11, Appl
36	3	75.0	4	15	US-10-025-514-33	Sequence 33, Appl
37	3	75.0	4	15	US-10-209-812-6	Sequence 6, Appli
38	3	75.0	4	15	US-10-028-075B-72	Sequence 72, Appl
39	3	75.0	4	15	US-10-104-693-6	Sequence 6, Appli
40	3	75.0	4	15	US-10-029-206A-72	Sequence 72, Appl
41	3	75.0	4	15	US-10-229-346-35	Sequence 35, Appl
42	3	75.0	4	15	US-10-229-346-36	Sequence 36, Appl
43	3	75.0	5	12	US-10-293-086-143	Sequence 143, App
44	3	75.0	5	12	US-10-352-786-124	Sequence 124, App
45	3	75.0	5	12	US-10-352-786-126	Sequence 126, App

ALIGNMENTS

RESULT 1

US-09-935-744-2

; Sequence 2, Application US/09935744

; Patent No. US20020137118A1

; GENERAL INFORMATION:

; APPLICANT: Inouye, Masayori

```

; APPLICANT: Shinde, Ujwal
; APPLICANT: Fu, Xuan
; TITLE OF INVENTION: Biologically Active Protein Folding Intermediates
; FILE REFERENCE: 266/223
; CURRENT APPLICATION NUMBER: US/09/935,744
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The sequence is part of a synthetic peptide that is used
as a sub
; OTHER INFORMATION: strate for determining the activation time of a stable
crosslinke
; OTHER INFORMATION: d intermediate conformer.
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(4)
; OTHER INFORMATION: Sequence is preceded by N-succinyl and followed by p-
nitroanilide
US-09-935-744-2

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Query Match          100.0%; Score 4; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      1 AAPL 4
        ||||
Db      1 AAPL 4

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RESULT 2
US-10-033-526-3
; Sequence 3, Application US/10033526
; Publication No. US20020147999A1
; GENERAL INFORMATION:
; APPLICANT: Robert W. Mahley
; APPLICANT: Yadong Huang
; TITLE OF INVENTION: Methods of Treating Disorders Related to
; TITLE OF INVENTION: APOE
; FILE REFERENCE: UCAL217
; CURRENT APPLICATION NUMBER: US/10/033,526
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 60/245,737
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-033-526-3

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Query Match 100.0%; Score 4; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
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Db 1 AAPL 4

RESULT 3

US-10-206-699-143

; Sequence 143, Application US/10206699
; Publication No. US20030100510A1
; GENERAL INFORMATION:
; APPLICANT: Sundaramoorthy, M.
; APPLICANT: Hudson, B.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NC1 Domain Hexamer
; FILE REFERENCE: MBHB 01-1017
; CURRENT APPLICATION NUMBER: US/10/206,699
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/308,523
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/351,289
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/366,854
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/385,362
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 143
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-206-699-143

Query Match 100.0%; Score 4; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPL 4
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Db 1 AAPL 4

RESULT 4

US-10-193-768-3

; Sequence 3, Application US/10193768
; Publication No. US20030109423A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Jun Ping
; APPLICANT: Cantley, Lewis C.
; APPLICANT: Yaffe, Michael
; APPLICANT: Fischer, Gunter
; TITLE OF INVENTION: INHIBITORS OF PHOSPHOSERINE AND
; TITLE OF INVENTION: PHOSPHOTHREONINE-PROLINE-SPECIFIC ISOMERASES

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; FILE REFERENCE: BIDMC97-02pA
; CURRENT APPLICATION NUMBER: US/10/193,768
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/08/988,842
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: synthetic nucleotide
; FEATURE:
; NAME/KEY: PHOSPHORYLATION
; LOCATION: (5)...(5)
US-10-193-768-3

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Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches      4; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

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```

Qy      1 AAPL 4
        ||||
Db      1 AAPL 4

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RESULT 5

US-09-842-543-1

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; Sequence 1, Application US/09842543
; Patent No. US20020010315A1
; GENERAL INFORMATION:
; APPLICANT: Gyorkos, et al.
; TITLE OF INVENTION: PEPTOID AND NONPEPTOID CONTAINING
; TITLE OF INVENTION: ALPHA-KETO SERINE PROTEASE INHIBITORS
; FILE REFERENCE: 361239-016A
; CURRENT APPLICATION NUMBER: US/09/842,543
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 09/325,512
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is a known commercially available
; OTHER INFORMATION: substrate for elastases.
; NAME/KEY: BLOCKED
; LOCATION: (1)...(1)
; OTHER INFORMATION: N-terminal Methoxysuccinyl group.
; NAME/KEY: BLOCKED
; LOCATION: (4)...(4)
; OTHER INFORMATION: C-terminal p-nitroaniline
US-09-842-543-1

```

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Query Match          75.0%; Score 3; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;

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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAP 3
|||
Db 1 AAP 3

RESULT 6

US-09-757-908A-14

; Sequence 14, Application US/09757908A
; Patent No. US20020052468A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell
; TITLE OF INVENTION: Disulfide Core Polypeptides
; FILE REFERENCE: 98-13D1
; CURRENT APPLICATION NUMBER: US/09/757,908A
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 09/326,039
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: US 60/088,136
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-757-908A-14

Query Match 75.0%; Score 3; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAP 3
|||
Db 1 AAP 3

RESULT 7

US-09-757-908A-15

; Sequence 15, Application US/09757908A
; Patent No. US20020052468A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell
; TITLE OF INVENTION: Disulfide Core Polypeptides
; FILE REFERENCE: 98-13D1
; CURRENT APPLICATION NUMBER: US/09/757,908A
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 09/326,039
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: US 60/088,136
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 4
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-757-908A-15

Query Match 75.0%; Score 3; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAP 3
|||
Db 1 AAP 3

RESULT 8

US-09-117-380B-1
; Sequence 1, Application US/09117380B
; Patent No. US20020119917A1
; GENERAL INFORMATION:
; APPLICANT: FRIDKIN, Matityahu
; APPLICANT: YAVIN, Eran J.
; TITLE OF INVENTION: ANTI-INFLAMMATORY PEPTIDES DERIVED FROM C-REACTIVE
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: FRIDKIN=1
; CURRENT APPLICATION NUMBER: US/09/117,380B
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: PCT/IL97/00032
; PRIOR FILING DATE: 1997-01-27
; PRIOR APPLICATION NUMBER: IL 116976
; PRIOR FILING DATE: 1996-01-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: The N-terminal Ala residue is modified with a
; OTHER INFORMATION: methoxysuccinyl group; the C-terminal Val residue
; OTHER INFORMATION: is modified with a nitroanilide group.
US-09-117-380B-1

Query Match 75.0%; Score 3; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAP 3
|||
Db 1 AAP 3

RESULT 9

US-09-117-380B-2
; Sequence 2, Application US/09117380B
; Patent No. US20020119917A1
; GENERAL INFORMATION:
; APPLICANT: FRIDKIN, Matityahu
; APPLICANT: YAVIN, Eran J.


```

; TITLE OF INVENTION: ANTI-INFLAMMATORY PEPTIDES DERIVED FROM C-REACTIVE
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: FRIDKIN=1
; CURRENT APPLICATION NUMBER: US/09/117,380B
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: PCT/IL97/00032
; PRIOR FILING DATE: 1997-01-27
; PRIOR APPLICATION NUMBER: IL 116976
; PRIOR FILING DATE: 1996-01-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The N-terminal Ala residue is modified with a
; OTHER INFORMATION: succinyl group; the C-terminal Phe residue is
; OTHER INFORMATION: modified with a nitroanilide group.
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-117-380B-2

```

```

Query Match          75.0%; Score 3; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches      3; Conservative    0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 AAP 3
        |||
Db      1 AAP 3

```

RESULT 10

US-09-935-744-1

```

; Sequence 1, Application US/09935744
; Patent No. US20020137118A1
; GENERAL INFORMATION:
; APPLICANT: Inouye, Masayori
; APPLICANT: Shinde, Ujwal
; APPLICANT: Fu, Xuan
; TITLE OF INVENTION: Biologically Active Protein Folding Intermediates
; FILE REFERENCE: 266/223
; CURRENT APPLICATION NUMBER: US/09/935,744
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The sequence is part of a synthetic peptide that is used
as a sub
; OTHER INFORMATION: strate for determining the activation time of a stable
crosslinke
; OTHER INFORMATION: d intermediate conformer.
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(4)

```

; OTHER INFORMATION: Sequence is preceded by N-succinyl and followed by p-nitroanilide
US-09-935-744-1

Query Match 75.0%; Score 3; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAP 3
|||
Db 1 AAP 3

RESULT 11

US-09-928-117-1

; Sequence 1, Application US/09928117
; Publication No. US20030060418A1
; GENERAL INFORMATION:
; APPLICANT: Cortech, Inc.
; APPLICANT: Gyorkos, Albert
; APPLICANT: Spruce, Lyle W.
; TITLE OF INVENTION: Serine Protease Inhibitors-Keto And
; TITLE OF INVENTION: Di-Keto And Containing Ring Systems
; FILE REFERENCE: 21E-CIP2
; CURRENT APPLICATION NUMBER: US/09/928,117
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US/08/985,298
; PRIOR FILING DATE: 1997-12-04
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: BLOCKED
; LOCATION: (0)...(0)
; OTHER INFORMATION: Sequence is a known commercially available
; OTHER INFORMATION: substrate for elastases
; FEATURE:
; NAME/KEY: BLOCKED
; LOCATION: (1)...(1)
; OTHER INFORMATION: N-terminal Msu
; FEATURE:
; NAME/KEY: BLOCKED
; LOCATION: (4)...(4)
; OTHER INFORMATION: C-terminal pNA
US-09-928-117-1

Query Match 75.0%; Score 3; DB 11; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAP 3
|||
Db 1 AAP 3

RESULT 12

US-09-876-904A-19

; Sequence 19, Application US/09876904A
 ; Publication No. US20030072794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BOULIKAS, TENI
 ; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
 THERAPEUTIC
 ; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
 PEPTIDE
 ; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
 ; FILE REFERENCE: TB-2002.00
 ; CURRENT APPLICATION NUMBER: US/09/876,904A
 ; CURRENT FILING DATE: 2001-06-08
 ; PRIOR APPLICATION NUMBER: US 60/210,925
 ; PRIOR FILING DATE: 2000-06-09
 ; NUMBER OF SEQ ID NOS: 629
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 19
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic fusogenic
 peptide
 ; FEATURE:
 ; OTHER INFORMATION: see specification as filed for detailed description of R-
 groups,
 ; OTHER INFORMATION: modifications and preferred embodiments
 US-09-876-904A-19

Query Match 75.0%; Score 3; DB 11; Length 4;
 Best Local Similarity 100.0%; Pred. No. 6.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAP 3
 |||
 Db 1 AAP 3

RESULT 13

US-10-373-794-2

; Sequence 2, Application US/10373794
 ; Publication No. US20030152564A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FRIDKIN, Matityahu
 ; APPLICANT: YAVIN, Eran
 ; TITLE OF INVENTION: ANTI-INFLAMMATORY PEPTIDES DERIVED FROM C-REACTIVE
 PROTEIN
 ; FILE REFERENCE: FRIDKIN=3
 ; CURRENT APPLICATION NUMBER: US/10/373,794
 ; CURRENT FILING DATE: 2003-02-27
 ; PRIOR APPLICATION NUMBER: US/09/446,868
 ; PRIOR FILING DATE: 2000-03-28
 ; PRIOR APPLICATION NUMBER: PCT/IL98/00302
 ; PRIOR FILING DATE: 1998-06-29

```

; PRIOR APPLICATION NUMBER: IL 121191
; PRIOR FILING DATE: 1997-06-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: The N-terminal Ala residue is modified with a
methoxysuccinyl moi
;   OTHER INFORMATION: ety and the C-terminal Val residue is modified with a
nitroanilid
;   OTHER INFORMATION: e moiety.
US-10-373-794-2

```

```

Query Match          75.0%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      1 AAP 3
        |||
Db      1 AAP 3

```

RESULT 14

```

US-10-373-794-3
; Sequence 3, Application US/10373794
; Publication No. US20030152564A1
; GENERAL INFORMATION:
; APPLICANT: FRIDKIN, Matityahu
; APPLICANT: YAVIN, Eran
; TITLE OF INVENTION: ANTI-INFLAMMATORY PEPTIDES DERIVED FROM C-REACTIVE
PROTEIN
; FILE REFERENCE: FRIDKIN=3
; CURRENT APPLICATION NUMBER: US/10/373,794
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US/09/446,868
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: PCT/IL98/00302
; PRIOR FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: IL 121191
; PRIOR FILING DATE: 1997-06-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic
;   FEATURE:
;   NAME/KEY: misc_feature

```

; OTHER INFORMATION: The N-terminal Ala residue is modified with a succinyl moiety and
; OTHER INFORMATION: the C-terminal Phe residue is modified with a nitroanilide moiety
; OTHER INFORMATION: y.
US-10-373-794-3

Query Match 75.0%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAP 3
|||
Db 1 AAP 3

RESULT 15

US-10-354-706-1
; Sequence 1, Application US/10354706
; Publication No. US20030176642A1
; GENERAL INFORMATION:
; APPLICANT: Gyorkos, et al.
; TITLE OF INVENTION: Peptoid and No. US20030176642A1peptoid Containing
; TITLE OF INVENTION: Alpha-Keto Serine Protease Inhibitors
; FILE REFERENCE: 2635A/139
; CURRENT APPLICATION NUMBER: US/10/354,706
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: 09/842,543
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 09/325,512
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is a known commercially available
; OTHER INFORMATION: substrate for elastases.
; FEATURE:
; NAME/KEY: BLOCKED
; LOCATION: (1)...(1)
; OTHER INFORMATION: N-terminal Methoxysuccinyl group.
; FEATURE:
; NAME/KEY: BLOCKED
; LOCATION: (4)...(4)
; OTHER INFORMATION: C-terminal p-nitroaniline.
US-10-354-706-1

Query Match 75.0%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAP 3
|||
Db 1 AAP 3

Search completed: December 30, 2003, 12:36:16
Job time : 21.2857 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 12:19:51 ; Search time 9.42857 Seconds
(without alignments)
40.799 Million cell updates/sec

Title: US-10-033-526-3
Perfect score: 4
Sequence: 1 AAPL 4

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 293

Minimum DB seq length: 4

Maximum DB seq length: 6

Post-processing: Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	3	75.0	5	2	JS0319		subesophageal gang
2	3	75.0	6	2	B60110		repetitive protein
3	2	50.0	4	2	A32039		tyrosine-melanocyt
4	2	50.0	4	2	A34626		RPCH-related neuro
5	2	50.0	5	2	B41225		copper resistance
6	2	50.0	5	2	B60274		major protein anti
7	2	50.0	5	2	PS0324		ribulose-bisphosph
8	2	50.0	5	2	S55237		zinc-binding prote
9	2	50.0	5	2	G37196		bradykinin-potenti
10	2	50.0	5	2	S11127		phosphoprotein, bo
11	2	50.0	6	2	S66195		alcohol dehydrogen
12	2	50.0	6	2	C22565		R-phycoerythrin be
13	2	50.0	6	2	A43766		28K ubiquitin-immu

14	2	50.0	6	2	B27696	contraction-inhibi
15	2	50.0	6	2	PT0280	Ig heavy chain CRD
16	2	50.0	6	2	PT0616	T-cell receptor be
17	2	50.0	6	4	S15596	orf 3 rara 5'-regi
18	1	25.0	4	2	S18401	thyroglobulin - do
19	1	25.0	4	2	A02147	phagocytosis-stimu
20	1	25.0	4	2	PL0140	carbon-monoxide de
21	1	25.0	4	2	PL0146	carbon-monoxide de
22	1	25.0	4	2	A48360	gamma subunit of P
23	1	25.0	4	2	S43014	hypothetical prote
24	1	25.0	4	2	B43848	cell surface adhes
25	1	25.0	4	2	I40505	hypothetical prote
26	1	25.0	4	2	T46627	hypothetical prote
27	1	25.0	4	2	S53508	starvation-induced
28	1	25.0	4	2	S17255	ribosomal protein
29	1	25.0	4	2	A27897	glucan 1,4-alpha-g
30	1	25.0	4	2	I38888	COI intron 16 prot
31	1	25.0	4	2	JQ1273	neuropeptide Antho
32	1	25.0	4	2	A35779	neuropeptide Antho
33	1	25.0	4	2	A32480	achatin-I - giant
34	1	25.0	4	2	I51049	metallothionein-A
35	1	25.0	4	2	S39390	myosin-light-chain
36	1	25.0	4	2	I61883	protamine P1 - ora
37	1	25.0	4	2	PT0240	Ig heavy chain CRD
38	1	25.0	4	2	PT0271	Ig heavy chain CRD
39	1	25.0	4	2	S43959	Ig mu chain V regi
40	1	25.0	4	2	A53284	T-cell receptor be
41	1	25.0	4	2	I54357	schwannomin - mous
42	1	25.0	4	2	PT0696	T-cell receptor be
43	1	25.0	4	2	PT0645	T-cell receptor be
44	1	25.0	4	2	PT0633	T-cell receptor be
45	1	25.0	4	2	PT0711	T-cell receptor be

ALIGNMENTS

RESULT 1

JS0319

subesophageal ganglion pentapeptide - house cricket

C;Species: Acheta domesticus (house cricket)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000

C;Accession: JS0319

R;Wicker, C.; Wicker, C.

Comp. Biochem. Physiol. C 88, 185-187, 1987

A;Title: Isolation and structure of a peptide isolated from the subesophageal ganglion of Acheta domesticus (orthoptera).

A;Reference number: JS0319

A;Accession: JS0319

A;Molecule type: protein

A;Residues: 1-5 <WIC>

Query Match 75.0%; Score 3; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 AAP 3

Db

2 AAP 4

RESULT 2

B60110

repetitive protein antigen 61 - Trypanosoma cruzi (fragment)

C;Species: Trypanosoma cruzi

C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 18-Jun-1993

C;Accession: B60110

R;Hoft, D.F.; Kim, K.S.; Otsu, K.; Moser, D.R.; Yost, W.J.; Blumin, J.H.;
Donelson, J.E.; Kirchhoff, L.V.

Infect. Immun. 57, 1959-1967, 1989

A;Title: Trypanosoma cruzi expresses diverse repetitive protein antigens.

A;Reference number: A60110; MUID:89277508; PMID:2659529

A;Accession: B60110

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-6 <HOF>

A;Note: this is an example of a five residue tandem repeat from this protein;
the actual protein sequence is not given in the paper

C;Keywords: tandem repeat

Query Match 75.0%; Score 3; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAP 3

Db

1 AAP 3

RESULT 3

A32039

tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000

C;Accession: A32039

R;Horvath, A.; Kastin, A.J.

J. Biol. Chem. 264, 2175-2179, 1989

A;Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting
factor 1 from bovine brain tissue.

A;Reference number: A32039; MUID:89123285; PMID:2563371

A;Accession: A32039

A;Molecule type: protein

A;Residues: 1-4 <HOR>

A;Experimental source: brain

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end

F;4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 50.0%; Score 2; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PL 4

Db

2 PL 3

RESULT 4

A34626

RPCH-related neuropeptide - ferruginous spindle

C;Species: *Fusinus ferrugineus* (ferruginous spindle)

C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993

C;Accession: A34626

R;Kuroki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.;
Minamitake, Y.; Muneoka, Y.

Biochem. Biophys. Res. Commun. 167, 273-279, 1990

A;Title: A molluscan neuropeptide related to the crustacean hormone, RPCH.

A;Reference number: A34626; MUID:90179762; PMID:2310394

A;Accession: A34626

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-4 <KUR>

C;Keywords: neuropeptide

Query Match 50.0%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AP 3

||

Db 1 AP 2

RESULT 5

B41225

copper resistance protein B - *Pseudomonas syringae* pv. tomato (fragment)

C;Species: *Pseudomonas syringae* pv. tomato

C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993

C;Accession: B41225

R;Cha, J.S.; Cooksey, D.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991

A;Title: Copper resistance in *Pseudomonas syringae* mediated by periplasmic and
outer membrane proteins.

A;Reference number: A41225; MUID:92020961; PMID:1924351

A;Accession: B41225

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-5 <CHA>

Query Match 50.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AA 2

||

Db 3 AA 4

RESULT 6

B60274

major protein antigen MPT32 - *Mycobacterium tuberculosis* (fragment)

C;Species: Mycobacterium tuberculosis
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C;Accession: B60274
R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A;Title: Isolation and partial characterization of major protein antigens in the culture fluid of Mycobacterium tuberculosis.
A;Reference number: A60274; MUID:91099989; PMID:1898899
A;Accession: B60274
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <NAG>

Query Match 50.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AP 3
||
Db 3 AP 4

RESULT 7

PS0324

ribulose-bisphosphate carboxylase activase III - rice (strain Nihonbare)
(fragment)

C;Species: Oryza sativa (rice)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 02-Jul-1998
C;Accession: PS0324
R;Tsugita, A.
submitted to JIPID, April 1993
A;Reference number: PS0206
A;Accession: PS0324
A;Molecule type: protein
A;Residues: 1-5 <TSU>
A;Experimental source: leaf, chlorophyll

Query Match 50.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AP 3
||
Db 3 AP 4

RESULT 8

S55237

zinc-binding protein ZBP14 - maize (fragment)

C;Species: Zea mays (maize)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C;Accession: S55237
R;Robinson, K.; Jones, D.; Howell, S.; Soneji, Y.; Martin, S.; Aitken, A.
Biochem. J. 307, 267-272, 1995
A;Title: Expression and characterization of maize ZBP14, a member of a new family of zinc-binding proteins.
A;Reference number: S55237; MUID:95234046; PMID:7717986

A;Accession: S55237
A;Molecule type: protein
A;Residues: 1-5 <ROB>

Query Match 50.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AA 2
||
Db 2 AA 3

RESULT 9

G37196

bradykinin-potentiating peptide 7 - island jararaca

C;Species: Bothrops insularis (island jararaca)

C;Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994

C;Accession: G37196

R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.

J. Protein Chem. 9, 221-227, 1990

A;Title: Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.

A;Reference number: A37196; MUID:90351557; PMID:2386615

A;Accession: G37196

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-5 <CIN>

C;Keywords: pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 50.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AP 3
||
Db 4 AP 5

RESULT 10

S11127

phosphoprotein, bone - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Mar-2000

C;Accession: S11127; S11128

R;Mikuni-Takagaki, Y.; Glimcher, M.J.

Biochem. J. 268, 585-591, 1990

A;Title: Post-translational processing of chicken bone phosphoproteins. Identification of the bone phosphoproteins of embryonic tibia.

A;Reference number: S11127; MUID:90303246; PMID:2363696

A;Accession: S11127

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-5 <MIK1>

A;Accession: S11128

A;Status: preliminary

A;Molecule type: protein
A;Residues: 'X',2-5 <MIK2>
C;Keywords: phosphoprotein

Query Match 50.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AP 3
||
Db 1 AP 2

RESULT 11

S66195

alcohol dehydrogenase (EC 1.1.1.1) class III low affinity form - cod (Gadus sp.)
(fragment)

C;Species: Gadus sp. (cod)

C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 12-Jun-1998

C;Accession: S66195

R;Hjelmqvist, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.;
Hendrickson, R.C.; Michel, H.; Shabanowitz, J.; Hunt, D.F.; Joernvall, H.
FEBS Lett. 367, 237-240, 1995

A;Title: Multiplicity of N-terminal structures of medium-chain alcohol
dehydrogenases. Mass-spectrometric analysis of plant, lower vertebrate and
higher vertebrate class I, II, and III forms of the enzyme.

A;Reference number: S66191; MUID:95331382; PMID:7607314

A;Accession: S66195

A;Molecule type: protein

A;Residues: 1-6 <HJE>

C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 50.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AA 2
||
Db 1 AA 2

RESULT 12

C22565

R-phycoerythrin beta-1 chain - red alga (Gastroclonium coulteri) (fragment)

C;Species: Gastroclonium coulteri

C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993

C;Accession: C22565

R;Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985

A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.

A;Reference number: A22565; MUID:85182601; PMID:3886644

A;Accession: C22565

A;Molecule type: protein

A;Residues: 1-6 <KLO>

Query Match 50.0%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AA 2
||
Db 2 AA 3

RESULT 13

A43766

28K ubiquitin-immunoreactive protein - inky cap (*Coprinus cinereus*) (fragment)

C;Species: *Coprinus cinereus*

C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 30-Sep-1993

C;Accession: A43766

R;Kanda, T.; Inoue, M.; Akiyama, M.

Biochimie 72, 355-359, 1990

A;Title: Purification and characterization of an ubiquitin-immuno-reactive protein localized in the cap of young basidiocarp in the basidiomycete *Coprinus cinereus*.

A;Reference number: A43766; MUID:91002724; PMID:1698461

A;Accession: A43766

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-6 <KAN>

Query Match 50.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AP 3
||
Db 1 AP 2

RESULT 14

B27696

contraction-inhibiting peptide II - blue mussel

C;Species: *Mytilus edulis* (blue mussel)

C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 08-Dec-1995

C;Accession: B27696

R;Hirata, T.; Kubota, I.; Iwasawa, N.; Takabatake, I.; Ikeda, T.; Muneoka, Y.

Biochem. Biophys. Res. Commun. 152, 1376-1382, 1988

A;Title: Structures and actions of *Mytilus* inhibitory peptides.

A;Reference number: A90142; MUID:88240357; PMID:3377776

A;Accession: B27696

A;Molecule type: protein

A;Residues: 1-6 <HIR>

C;Keywords: amidated carboxyl end

F;6/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 50.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AP 3
||
Db 2 AP 3

RESULT 15

PT0280

Ig heavy chain CRD3 region (clone 4-91B) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PT0280

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain
diversity and joining segments in adult human peripheral blood B lymphocytes.

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0280

A;Molecule type: DNA

A;Residues: 1-6 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 50.0%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AP 3

||

Db 5 AP 6

Search completed: December 30, 2003, 12:24:27

Job time : 9.42857 secs

OM protein - protein search, using sw model

Run on: December 30, 2003, 12:16:41 ; Search time 6.57143 Seconds
 (without alignments)
 28.625 Million cell updates/sec

Title: US-10-033-526-3
 Perfect score: 4
 Sequence: 1 AAPL 4

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 47

Minimum DB seq length: 4

Maximum DB seq length: 6

Post-processing: Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3	75.0	5	1	SUGA_ACHDO	P19991 acheta dome
2	2	50.0	5	1	BPP7_BOTIN	P30425 bothrops in
3	2	50.0	6	1	CIP2_MYTED	P13737 mytilus edu
4	2	50.0	6	1	VP19_HSV1K	P23210 herpes simp
5	1	25.0	4	1	ACH1_ACHFU	P35904 achatina fu
6	1	25.0	4	1	DCML_PSECH	P19916 pseudomonas
7	1	25.0	4	1	DCMS_PSECH	P19918 pseudomonas
8	1	25.0	4	1	FAR3_HIRME	P42562 hirudo medi
9	1	25.0	4	1	FFKA_ANTEL	P58705 anthopleura
10	1	25.0	4	1	FLRF_HIRME	P42561 hirudo medi
11	1	25.0	4	1	FLRN_ANTEL	P58707 anthopleura
12	1	25.0	4	1	RM01_YEAST	P36515 saccharomyc
13	1	25.0	4	1	TUFT_HUMAN	P01858 homo sapien
14	1	25.0	5	1	AL14_CARMA	P81817 carcinus ma
15	1	25.0	5	1	BIOB_CITFR	P12997 citrobacter
16	1	25.0	5	1	EI03_LITRU	P82099 litoria rub
17	1	25.0	5	1	PAP2_PARMA	P81864 pardachirus

18	1	25.0	5	1	PRCT_PERAM	P01373	periplaneta
19	1	25.0	5	1	RE11_LITRU	P82070	litoria rub
20	1	25.0	5	1	RE21_LITRU	P82071	litoria rub
21	1	25.0	6	1	ACPH_RABIT	P25154	oryctolagus
22	1	25.0	6	1	CIP1_MYTED	P13736	mytilus edu
23	1	25.0	6	1	EI01_LITRU	P82096	litoria rub
24	1	25.0	6	1	LOK1_LOCFI	P41491	locusta mig
25	1	25.0	6	1	OVM_LEPDE	P42985	leptinotars
26	1	25.0	6	1	TMOF_SARBU	P41495	sarcophaga
27	1	25.0	6	1	TRPI_PSEPU	P36414	pseudomonas
28	1	25.0	6	1	UN06_CLOPA	P81351	clostridium
29	0	0.0	4	1	EOSI_HUMAN	P02731	homo sapien
30	0	0.0	4	1	FAR4_HIRME	P42563	hirudo medi
31	0	0.0	4	1	FMRF_MACNI	P01162	macrocallis
32	0	0.0	4	1	FYRI_ANTEI	P58706	anthopleura
33	0	0.0	4	1	OCP1_OCTMI	P58648	octopus min
34	0	0.0	4	1	OCP3_OCTMI	P58649	octopus min
35	0	0.0	5	1	BIOA_CITFR	P13071	citrobacter
36	0	0.0	5	1	EI04_LITRU	P82100	litoria rub
37	0	0.0	5	1	FARP_ARTTR	P41853	artioposthi
38	0	0.0	5	1	PSK_DAUCA	P58261	daucus caro
39	0	0.0	5	1	RE31_LITRU	P82072	litoria rub
40	0	0.0	5	1	RE32_LITRU	P82073	litoria rub
41	0	0.0	5	1	TPIS_CANFA	P54714	canis famil
42	0	0.0	5	1	TRM3_ECOLI	P13973	escherichia
43	0	0.0	5	1	UC22_MAIZE	P80628	zea mays (m
44	0	0.0	5	1	UF01_MOUSE	P38639	mus musculu
45	0	0.0	5	1	UXA4_CHLTR	P38005	chlamydia t

ALIGNMENTS

RESULT 1

SUGA_ACHDO

ID SUGA_ACHDO STANDARD; PRT; 5 AA.

AC P19991;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Suboesophageal ganglion pentapeptide.

OS Acheta domesticus (House cricket).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;

OC Acheta.

OX NCBI_TaxID=6997;

RN [1]

RP SEQUENCE.

RA Wicker C., Wicker C.;

RT "Isolation and structure of a peptide isolated from the

RT suboesophageal ganglion of Acheta domesticus (orthoptera).";

RL Comp. Biochem. Physiol. 88C:185-187(1987).

CC -!- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBOESOPHAGEAL

CC GANGLIA.

DR PIR; JS0319; JS0319.

SQ SEQUENCE 5 AA; 476 MW; 69D76DDDDDB00000 CRC64;

Query Match 75.0%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAP 3
|||
Db 2 AAP 4

RESULT 2

BPP7_BOTIN

ID BPP7_BOTIN STANDARD; PRT; 5 AA.
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; G37196; G37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AP 3
||
Db 4 AP 5

RESULT 3

CIP2_MYTED

ID CIP2_MYTED STANDARD; PRT; 6 AA.
AC P13737;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Contraction-inhibiting peptide II (MIP II).

OS *Mytilus edulis* (Blue mussel).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloida;
 OC Mytiloidea; Mytilidae; Mytilus.
 OX NCBI_TaxID=6550;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pedal ganglion;
 RX MEDLINE=88240357; PubMed=3377776;
 RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
 RT "Structures and actions of *Mytilus* inhibitory peptides.";
 RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
 CC -!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
 CC MUSCLES.
 CC -!- SIMILARITY: TO MIP I.
 DR PIR; B27696; B27696.
 KW Hormone; Amidation.
 FT MOD_RES 6 6 AMIDATION.
 SQ SEQUENCE 6 AA; 621 MW; 72C9C6876DD81000 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AP 3
 ||
 Db 2 AP 3

RESULT 4

VP19_HSV1K

ID VP19_HSV1K STANDARD; PRT; 6 AA.

AC P23210;

DT 01-NOV-1991 (Rel. 20, Created)

DT 01-NOV-1991 (Rel. 20, Last sequence update)

DT 01-DEC-1992 (Rel. 24, Last annotation update)

DE Capsid assembly and DNA maturation protein (Virion protein UL38)

DE (Capsid protein VP19C) (Fragment).

GN UL38.

OS Herpes simplex virus (type 1 / strain KOS).

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Alphaherpesvirinae; Simplexvirus.

OX NCBI_TaxID=10306;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91101287; PubMed=1846198;

RA Flanagan W.M., Papavassiliou A.G., Rice M., Hecht L.B.,

RA Silverstein S., Wagner E.K.;

RT "Analysis of the herpes simplex virus type 1 promoter controlling the

RT expression of UL38, a true late gene involved in capsid assembly.";

RL J. Virol. 65:769-786(1991).

CC -!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE

CC EMBEDDED. BINDS DNA.

CC -!- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.

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DR EMBL; M57646; AAA45830.1; -.
KW Capsid assembly; Coat protein; DNA-binding.
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PL 4
||
Db 5 PL 6

RESULT 5

ACH1_ACHFU

ID ACH1_ACHFU STANDARD; PRT; 4 AA.
AC P35904;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Achatin-I.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
RC STRAIN=Ferussac; TISSUE=Ganglion;
RX MEDLINE=89273551; PubMed=2597281;
RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
RT fulica Ferussac containing a D-amino acid residue.";
RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
RN [2]
RP CHARACTERIZATION.
RC STRAIN=Ferussac; TISSUE=Heart atrium;
RX MEDLINE=91264856; PubMed=1675568;
RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
RT "Purification of achatin-I from the atria of the African giant snail,
RT Achatina fulica, and its possible function.";
RL Biochem. Biophys. Res. Commun. 177:847-853(1991).
RN [3]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=93014529; PubMed=1399265;
RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
RA Iwashita T., Nomoto K.;
RT "Crystal structure and molecular conformation of achatin-I
RT (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a

RT D-amino acid residue.";
 RL Int. J. Pept. Protein Res. 39:258-264(1992).
 CC -!- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY
 CC AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY
 CC NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE
 CC HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.
 DR PIR; A32480; A32480.
 KW Hormone; D-amino acid.
 FT MOD_RES 2 2 D-PHENYLALANINE.
 SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;

Query Match 25.0%; Score 1; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 3 A 3

RESULT 6

DCML_PSECH

ID DCML_PSECH STANDARD; PRT; 4 AA.
 AC P19916;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO
 DE dehydrogenase subunit L) (CO-DH L) (Fragment).
 GN CUTL.
 OS Pseudomonas carboxydohydrogena.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae.
 OX NCBI_TaxID=290;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90055678; PubMed=2818128;
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 RT carboxydotrophic bacteria.";
 RL Arch. Microbiol. 152:335-341(1989).
 CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
 CC dioxide.
 CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
 CC acceptor.
 CC -!- COFACTOR: Molybdenum (molybdopterin).
 CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 CC SMALL.
 DR PIR; PL0140; PL0140.
 KW Oxidoreductase; Molybdenum.
 FT NON_TER 4 4
 SQ SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;

Query Match 25.0%; Score 1; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 P 3
 |
 Db 4 P 4

RESULT 7

DCMS_PSECH
 ID DCMS_PSECH STANDARD; PRT; 4 AA.
 AC P19918;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO
 DE dehydrogenase subunit S) (CO-DH S) (Fragment).
 GN CUTS.
 OS Pseudomonas carboxydohydrogena.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae.
 OX NCBI_TaxID=290;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90055678; PubMed=2818128;
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 RT carboxydotrophic bacteria.";
 RL Arch. Microbiol. 152:335-341(1989).
 CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
 CC dioxide.
 CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
 CC acceptor.
 CC -!- COFACTOR: BINDS TWO 2FE-2S CLUSTERS.
 CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 CC SMALL.
 DR PIR; PL0146; PL0146.
 KW Oxidoreductase; Metal-binding; Iron-sulfur; Iron; 2Fe-2S.
 FT NON_TER 4 4
 SQ SEQUENCE 4 AA; 420 MW; 6DD33DD6F0000000 CRC64;

Query Match 25.0%; Score 1; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 2 A 2

RESULT 8

FAR3_HIRME
 ID FAR3_HIRME STANDARD; PRT; 4 AA.
 AC P42562;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide YLRF-amide.
 OS Hirudo medicinalis (Medicinal leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;

OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92195954; PubMed=1686933;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech.";
 RL Peptides 12:897-908(1991).
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 4 4 AMIDATION.
 SQ SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;

Query Match 25.0%; Score 1; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
 |
 Db 2 L 2

RESULT 9

FFKA_ANTEL

ID FFKA ANTEL STANDARD; PRT; 4 AA.
 AC P58705;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Antho-KAamide.
 OS Anthopleura elegantissima (Sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nynanthaeae; Actiniidae; Anthopleura.
 OX NCBI_TaxID=6110;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92028852; PubMed=1681803;
 RA Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
 RT "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a
 RT novel neuropeptide from sea anemones.";
 RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
 RN [2]
 RP FUNCTION.
 RX MEDLINE=93391436; PubMed=8397415;
 RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
 RT "The expansion behaviour of sea anemones may be coordinated by two
 RT inhibitory neuropeptides, Antho-KAamide and Antho-RIamide.";
 RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
 CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle
 CC groups. May be involved in the expansion phase of feeding
 CC behaviour in sea anemones.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Neuron-specific.
 DR PIR; JQ1273; JQ1273.
 KW Neuropeptide; Amidation.
 FT MOD_RES 1 1 L-3-PHENYLLACTYL.

FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 512 MW; 6DD339C9A0000000 CRC64;

Query Match 25.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 4 A 4

RESULT 10

FLRF_HIRME

ID FLRF_HIRME STANDARD; PRT; 4 AA.
AC P42561;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FLRFamide.
OS Hirudo medicinalis (Medicinal leech), and
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421, 27815;
RN [1]
RP SEQUENCE.
RC SPECIES=H.medicinalis;
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of RFamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
RN [2]
RP SEQUENCE.
RC SPECIES=H.trivolvis; TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
trivolvis.";
RL Peptides 15:31-36(1994).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;

Query Match 25.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4
|
Db 2 L 2

RESULT 11

FLRN_ATEL

ID FLRN_ANTEL STANDARD; PRT; 4 AA.
AC P58707;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Antho-RNamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynantheae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RX MEDLINE=90319122; PubMed=1973541;
RA Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
RA Reinscheid R.K., Nothacker H.-P., Staley A.L.;
RT "Isolation of L-3-phenyllactyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea
RT anemone neuropeptide containing an unusual amino-terminal blocking
RT group.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Neuron-specific.
CC -!- MASS SPECTROMETRY: MW=549.3; METHOD=FAB.
DR PIR; A35779; A35779.
KW Neuropeptide; Amidation.
FT MOD_RES 1 1 L-3-PHENYLLACTYL.
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 549 MW; 64540729A0000000 CRC64;

Query Match 25.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4
|
Db 2 L 2

RESULT 12

RM01_YEAST

ID RM01_YEAST STANDARD; PRT; 4 AA.
AC P36515;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Mitochondrial 60S ribosomal protein L1 (YmL1) (Fragment).
GN MRPL1.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RX MEDLINE=91285106; PubMed=2060626;
RA Grohmann L., Graack H.-R., Kruff V., Choli T., Goldschmidt-Reisin S.,
RA Kitakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal
RT subunit from yeast mitochondria.";

RL FEBS Lett. 284:51-56(1991).
DR PIR; S17255; S17255.
DR SGD; L0002681; MRPL1.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000 CRC64;

Query Match 25.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 P 3
|
Db 4 P 4

RESULT 13

TUFT_HUMAN

ID TUFT_HUMAN STANDARD; PRT; 4 AA.
AC P01858;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phagocytosis-stimulating peptide (Tuftsin).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72187087; PubMed=4112769;
RA Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.;
RT "The characteristics, isolation and synthesis of the phagocytosis
RT stimulating peptide tuftsin.";
RL Biochem. Biophys. Res. Commun. 47:172-179(1972).
RN [2]
RP IMMUNOGLOBULIN CLASS.
RX MEDLINE=68091045; PubMed=4169272;
RA Fidalgo B.V., Najjar V.A.;
RT "The physiological role of the lymphoid system. VI. The stimulatory
RT effect of leucophilic gamma globulin (leucokinin) on the phagocytic
RT activity of human polymorphonuclear leucocyte.";
RL Biochemistry 6:3386-3392(1967).
CC -!- MISCELLANEOUS: AN IGG (CALLED LEUCOKININ) BINDS REVERSIBLY TO THE
CC CELL MEMBRANE OF NEUTROPHILS IN THE BLOOD. LEUCOKININASE ON THE
CC MEMBRANE RELEASES THE ACTIVE PEPTIDE TUFTSIN FROM THE GAMMA CHAIN.
CC TUFTSIN IS ESSENTIAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTIC
CC ACTIVITY OF NEUTROPHILS.
DR PIR; A02147; A02147.
DR MIM; 191150; -.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006909; P:phagocytosis; NAS.
SQ SEQUENCE 4 AA; 501 MW; 74176321C0000000 CRC64;

Query Match 25.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 P 3
|
Db 3 P 3

RESULT 14

AL14_CARMA

ID AL14_CARMA STANDARD; PRT; 5 AA.
AC P81817;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 14.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 5 5 AMIDATION (POTENTIAL).
SQ SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;

Query Match 25.0%; Score 1; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4
|
Db 5 L 5

RESULT 15

BIOB_CITFR

ID BIOB_CITFR STANDARD; PRT; 5 AA.
AC P12997;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Biotin synthase (EC 2.8.1.6) (Biotin synthetase) (Fragment).
GN BIOB.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=89006280; PubMed=2971595;
 RA Shiuan D., Campbell A.;
 RT "Transcriptional regulation and gene arrangement of Escherichia coli,
 RT Citrobacter freundii and Salmonella typhimurium biotin operons.";
 RL Gene 67:203-211(1988).
 CC -!- CATALYTIC ACTIVITY: Dethiobiotin + sulfur = biotin.
 CC -!- PATHWAY: Biotin biosynthesis; last step.
 CC -!- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL; M21922; -; NOT_ANNOTATED_CDS.
 DR PIR; I40698; I40698.
 KW Biotin biosynthesis; Iron-sulfur; Transferase.
 FT NON_TER 5 5
 SQ SEQUENCE 5 AA; 532 MW; 75A5B1EDD6F00000 CRC64;

Query Match 25.0%; Score 1; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 2 A 2

Search completed: December 30, 2003, 12:23:40
 Job time : 6.57143 secs

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OM protein - protein search, using sw model

Run on: December 30, 2003, 12:20:27 ; Search time 22.8571 Seconds
(without alignments)
45.159 Million cell updates/sec

Title: US-10-033-526-3
Perfect score: 4
Sequence: 1 AAPL 4

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 4
Maximum DB seq length: 6

Post-processing: Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					
No.	Score	Match	Length	DB	ID	Description

1	2	50.0	5	13	P83308	P83308 gallus gall
2	1	25.0	4	11	Q08433	Q08433 rattus sp.
3	1	25.0	5	10	Q99007	Q99007 hordeum vul
4	1	25.0	6	10	P82181	P82181 spinacia ol
5	1	25.0	6	10	P82541	P82541 spinacia ol
6	1	25.0	6	10	P82182	P82182 spinacia ol
7	0	0.0	5	2	P83073	P83073 bacillus ce

ALIGNMENTS

RESULT 1

P83308

ID P83308 PRELIMINARY; PRT; 5 AA.
AC P83308;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE FMRFamide-like neuropeptide (LPLRF-amide).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RX PubMed=6137771;
RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
RT "A novel active pentapeptide from chicken brain identified by
RT antibodies to FMRFamide.";
RL Nature 305:328-330(1983).
CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 50.0%; Score 2; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PL 4
||
Db 2 PL 3

RESULT 2

Q08433

ID Q08433 PRELIMINARY; PRT; 4 AA.
AC Q08433;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Bilirubin UDP-glucuronosyltransferase (Fragment).
OS Rattus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Gunn;
 RX MEDLINE=91282758; PubMed=1840486;
 RA Sato H., Aono S., Kashiwamata S., Koiwai O.;
 RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
 RT hyperbilirubinemic Gunn rat.";
 RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
 DR EMBL; S38636; AAB19259.1; -.
 KW Transferase.
 FT NON_TER 1 1
 SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 25.0%; Score 1; DB 11; Length 4;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4
 |
 Db 3 L 3

RESULT 3

Q99007

ID Q99007 PRELIMINARY; PRT; 5 AA.
 AC Q99007;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Alpha amylase (Fragment).
 GN AMY1 GENE.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91329704; PubMed=1831055;
 RA Jacobsen J.V., Close T.J.;
 RT "Control of transient expression of chimaeric genes by gibberellic
 RT acid and abscisic acid in protoplasts prepared from mature barley
 RT aleurone layers.";
 RL Plant Mol. Biol. 16:713-721(1991).
 DR EMBL; X54643; CAA38455.1; -.
 FT NON_TER 5 5
 SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;

Query Match 25.0%; Score 1; DB 10; Length 5;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |

Db

2 A 2

RESULT 4

P82181

ID P82181 PRELIMINARY; PRT; 6 AA.
AC P82181;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Chloroplast 50S ribosomal protein L10 beta (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. ALWARO; TISSUE=Leaf;
RX MEDLINE=20435798; PubMed=10874046;
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro; IPR001790; Ribosomal_L10.
DR InterPro; IPR002363; Ribosomal_L10eub.
DR Pfam; PF00466; Ribosomal_L10; PARTIAL.
DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 25.0%; Score 1; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 A 1
|
Db 1 A 1

RESULT 5

P82541

ID P82541 PRELIMINARY; PRT; 6 AA.
AC P82541;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Chloroplast 30S ribosomal protein S19 beta (Fragment).
OS Spinacia oleracea (Spinach).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC STRAIN=cv. ALWARO; TISSUE=Leaf;
 RX MEDLINE=20435797; PubMed=10874039;
 RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;
 RT "The plastid ribosomal proteins. Identification of all the proteins in
 RT the small subunit of an organelle ribosome (chloroplast).";
 RL J. Biol. Chem. 37:28455-28465(2000).
 CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -!- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.
 CC -!- MASS SPECTROMETRY: MW=10495; METHOD=MALDI.
 CC -!- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PI. S19 BETA
 CC FORM IS THE MINOR BASIC FORM.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 KDA.
 CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro; IPR002222; Ribosomal_S19.
 DR Pfam; PF00203; Ribosomal_S19; PARTIAL.
 DR PRINTS; PR00975; RIBOSOMALS19; PARTIAL.
 DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 FT NON_TER 6 6
 SQ SEQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;

Query Match 25.0%; Score 1; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4
 |
 Db 4 L 4

RESULT 6

P82182

ID P82182 PRELIMINARY; PRT; 6 AA.
 AC P82182;
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Chloroplast 50S ribosomal protein L10 gamma (Fragment).
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. ALWARO; TISSUE=Leaf;
 RX MEDLINE=20435798; PubMed=10874046;
 RA Yamaguchi K., Subramanian A.R.;
 RT "The plastid ribosomal proteins. Identification of all the proteins in
 RT the 50 S subunit of an organelle ribosome (chloroplast).";

RL J. Biol. Chem. 275:28466-28482(2000).
 CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
 CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro; IPR001790; Ribosomal_L10.
 DR InterPro; IPR002363; Ribosomal_L10eub.
 DR Pfam; PF00466; Ribosomal_L10; PARTIAL.
 DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 FT NON_TER 6 6
 SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 25.0%; Score 1; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 A 1
 |
 Db 1 A 1

RESULT 7

P83073

ID P83073 PRELIMINARY; PRT; 5 AA.
 AC P83073;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE 88 kDa protein (Fragment).
 OS Bacillus cereus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1396;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=NCIMB 11796;
 RA Browne N., Dowds B.C.A.;
 RL Submitted (JUL-2001) to the SWISS-PROT data bank.
 FT NON_TER 5 5
 SQ SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;

Query Match 0.0%; Score 0; DB 2; Length 5;
 Best Local Similarity 0.0%; Pred. No. 8.3e+05;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 A 1
 Db 1 M 1

Search completed: December 30, 2003, 12:25:59
 Job time : 22.8571 secs

OM protein - protein search, using sw model

Run on: December 30, 2003, 12:21:17 ; Search time 15.8571 Seconds
 (without alignments)
 16.010 Million cell updates/sec

Title: US-10-033-526-4
 Perfect score: 6
 Sequence: 1 AAAAPF 6

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 36631

Minimum DB seq length: 4

Maximum DB seq length: 6

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
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 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	5	83.3	6	1	US-07-960-510-8	Sequence 8, Appli
2	4	66.7	4	1	US-07-973-335-1	Sequence 1, Appli
3	4	66.7	4	1	US-08-155-331-19	Sequence 19, Appl
4	4	66.7	4	1	US-08-004-643C-2	Sequence 2, Appli
5	4	66.7	4	1	US-08-462-456-5	Sequence 5, Appli
6	4	66.7	4	1	US-07-972-007-34	Sequence 34, Appl
7	4	66.7	4	1	US-08-246-941-1	Sequence 1, Appli
8	4	66.7	4	1	US-08-351-058A-2	Sequence 2, Appli
9	4	66.7	4	1	US-08-282-860-1	Sequence 1, Appli
10	4	66.7	4	1	US-08-407-000-6	Sequence 6, Appli
11	4	66.7	4	1	US-07-890-422B-28	Sequence 28, Appl

12	4	66.7	4	1	US-08-276-936A-2	Sequence 2, Appli
13	4	66.7	4	1	US-08-345-820B-2	Sequence 2, Appli
14	4	66.7	4	1	US-08-544-143A-3	Sequence 3, Appli
15	4	66.7	4	1	US-08-397-602A-9	Sequence 9, Appli
16	4	66.7	4	1	US-08-437-029-5	Sequence 5, Appli
17	4	66.7	4	1	US-08-424-022-19	Sequence 19, Appl
18	4	66.7	4	1	US-08-439-534-10	Sequence 10, Appl
19	4	66.7	4	1	US-08-209-747-55	Sequence 55, Appl
20	4	66.7	4	1	US-08-434-959-3	Sequence 3, Appli
21	4	66.7	4	1	US-08-434-959-4	Sequence 4, Appli
22	4	66.7	4	1	US-08-434-959-5	Sequence 5, Appli
23	4	66.7	4	1	US-08-434-959-6	Sequence 6, Appli
24	4	66.7	4	1	US-08-460-343B-56	Sequence 56, Appl
25	4	66.7	4	1	US-08-067-180B-2	Sequence 2, Appli
26	4	66.7	4	1	US-08-458-298-55	Sequence 55, Appl
27	4	66.7	4	1	US-08-777-208-2	Sequence 2, Appli
28	4	66.7	4	1	US-08-647-618-34	Sequence 34, Appl
29	4	66.7	4	1	US-08-398-028B-56	Sequence 56, Appl
30	4	66.7	4	1	US-08-470-837-3	Sequence 3, Appli
31	4	66.7	4	2	US-08-722-268-2	Sequence 2, Appli
32	4	66.7	4	2	US-08-504-265B-56	Sequence 56, Appl
33	4	66.7	4	2	US-08-439-005-10	Sequence 10, Appl
34	4	66.7	4	2	US-08-698-575E-2	Sequence 2, Appli
35	4	66.7	4	2	US-08-424-017B-19	Sequence 19, Appl
36	4	66.7	4	2	US-08-685-152-2	Sequence 2, Appli
37	4	66.7	4	2	US-08-751-070B-4	Sequence 4, Appli
38	4	66.7	4	3	US-09-069-823-2	Sequence 2, Appli
39	4	66.7	4	3	US-09-060-011-1	Sequence 1, Appli
40	4	66.7	4	3	US-09-076-460-1	Sequence 1, Appli
41	4	66.7	4	3	US-08-950-618-3	Sequence 3, Appli
42	4	66.7	4	3	US-08-950-618-18	Sequence 18, Appl
43	4	66.7	4	3	US-08-950-618-31	Sequence 31, Appl
44	4	66.7	4	3	US-09-120-365-101	Sequence 101, App
45	4	66.7	4	3	US-08-814-836-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1

US-07-960-510-8

; Sequence 8, Application US/07960510

; Patent No. 5705362

; GENERAL INFORMATION:

; APPLICANT: BONEKAMP, ALFONSUSJOHANNES

; APPLICANT: VAN TILBORG E., MARCELLIS W.

; TITLE OF INVENTION: MODIFIED SIGNAL SEQUENCES

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 2000 Pennsylvania Ave., Suite 5500

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20006-1888

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/960,510
;      FILING DATE:  19921013
;      CLASSIFICATION:  435
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20034.00
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;      TELEX:  90-4030
;      INFORMATION FOR SEQ ID NO:  8:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-07-960-510-8

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Query Match          83.3%;  Score 5;  DB 1;  Length 6;
Best Local Similarity 100.0%;  Pred. No. 2.5e+05;
Matches      5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

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Qy      1 AAAAP 5
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Db      2 AAAAP 6

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RESULT 2

US-07-973-335-1

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; Sequence 1, Application US/07973335
; Patent No. 5338547
; GENERAL INFORMATION:
; APPLICANT:  Kennedy and Szuhaj
; TITLE OF INVENTION:  No. 5338547el Bowman-Birk Inhibitor
; TITLE OF INVENTION:  Product For Use As An Anticarcinogenesis Agent
; NUMBER OF SEQUENCES:  1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Woodcock Washburn Kurtz
; ADDRESSEE:  Mackiewicz & No. 5338547ris
; STREET:  One Liberty Place - 46th Floor
; CITY:  Philadelphia
; STATE:  PA
; COUNTRY:  USA
; ZIP:  19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER:  IBM PS/2
; OPERATING SYSTEM:  PC-DOS
; SOFTWARE:  WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/07/973,335
; FILING DATE:  19921102

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; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 824,719
; FILING DATE: January 17, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 579,155
; FILING DATE: September 6, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: UPSC-0003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-973-335-1

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Query Match          66.7%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      3 AAPF 6
        ||||
Db      1 AAPF 4

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```

RESULT 3
US-08-155-331-19
; Sequence 19, Application US/08155331
; Patent No. 5441931
; GENERAL INFORMATION:
; APPLICANT: Foster, Donald C
; APPLICANT: Sprecher, Cindy
; APPLICANT: No. 5441931ris, Kjeld
; TITLE OF INVENTION: NOVEL HUMAN AMYLOID PROTEIN PRECURSOR
; TITLE OF INVENTION: HOMOLOG AND KUNITZ-TYPE INHIBITOR
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 4225 Roosevelt Way, N.E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/155,331
; FILING DATE:
; CLASSIFICATION: 435

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/985,692
; FILING DATE: 02-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31-684
; REFERENCE/DOCKET NUMBER: 92-21C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-547-8080 ext 322
; TELEFAX: 206-548-2329
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..4
; OTHER INFORMATION: /label= ALA-1
; OTHER INFORMATION: /note= "Amino terminal alanine residue is capped
; OTHER INFORMATION: with a succinyl group"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..4
; OTHER INFORMATION: /label= Phe-4
; OTHER INFORMATION: /note= "Carboxyl-terminal phenylalanine resudue is
; OTHER INFORMATION: capped with p-nitroanil..."
US-08-155-331-19

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Query Match          66.7%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      3 AAPF 6
        ||||
Db      1 AAPF 4

```

RESULT 4

US-08-004-643C-2

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; Sequence 2, Application US/08004643C
; Patent No. 5480779
; GENERAL INFORMATION:
; APPLICANT: Gunter Fischer & Gerhard K llerz
; TITLE OF INVENTION: Cyclosporine Assay
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gunter Fischer et al. c/o G. P. Katona
; STREET: 230 Park Avenue, Room 2200
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10169
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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;      COMPUTER:  IBM pc compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  conf. to Patentin Release #1.0, Ver.#1.25
; CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/004,643C
;      FILING DATE:  12 January 1993
;      CLASSIFICATION:  435
; PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  703,590
;      FILING DATE:  20 May 1991
;      APPLICATION NUMBER:  398,092
;      FILING DATE:  24 August 1989
;      APPLICATION NUMBER:  DD WP 601 F/319 577W
;      FILING DATE:  07 September 1988
; ATTORNEY/AGENT INFORMATION:
;      NAME:  Katona, Gabriel P.
;      REGISTRATION NUMBER:  20,829
;      REFERENCE/DOCKET NUMBER:  691-003
; TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)986-3377
;      TELEFAX:  (212)986-6126
;      TELEX:
; INFORMATION FOR SEQ ID NO:  2:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acid residues
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-004-643C-2

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Query Match          66.7%;  Score 4;  DB 1;  Length 4;
Best Local Similarity 100.0%;  Pred. No. 2.5e+05;
Matches      4;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      3 AAPF 6
        ||||
Db      1 AAPF 4

```

RESULT 5

US-08-462-456-5

```

; Sequence 5, Application US/08462456
; Patent No. 5510333
; GENERAL INFORMATION:
;   APPLICANT:  Angelastro, Michael R
;   APPLICANT:  Bey, Philippe
;   APPLICANT:  Doherty, Niall S
;   APPLICANT:  Janusz, Michael J
;   APPLICANT:  Mehdi, Shujaath
;   APPLICANT:  Peet, No. 5510333ton P
;   TITLE OF INVENTION:  Inhibitors of Cathepsin G and Elastase
;   TITLE OF INVENTION:  for Preventing Connective Tissue Degradation
;   NUMBER OF SEQUENCES:  18
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Marion Merrell Dow Inc.
;   STREET:  2110 East Galbraith Rd.
;   CITY:  Cincinnati P. O. Box 156300

```



```

; STATE: Ohio
; COUNTRY: USA
; ZIP: 45215-6300
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,456
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/342,999
; FILING DATE:
; APPLICATION NUMBER: US/08/222,552
; FILING DATE:
; APPLICATION NUMBER: US/07/987,587
; FILING DATE:
; APPLICATION NUMBER: US/07/704,499
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Nesbitt, Stephen L
; REGISTRATION NUMBER: 28,981
; REFERENCE/DOCKET NUMBER: M01593
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (513) 948-7965
; TELEFAX: (513) 948-7961
; TELEX: 214320
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-462-456-5

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Query Match          66.7%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      3 AAPF 6
        ||||
Db      1 AAPF 4

```

RESULT 6

US-07-972-007-34

; Sequence 34, Application US/07972007

; Patent No. 5527681

; GENERAL INFORMATION:

; APPLICANT: Holmes, Christopher P.

; TITLE OF INVENTION: Cyclic and Substituted Immobilized

; TITLE OF INVENTION: Molecular Synthesis

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend

```

; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/972,007
; FILING DATE: 19921105
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5527681viel, Vernon A.
; REGISTRATION NUMBER: 32,483
; REFERENCE/DOCKET NUMBER: 11509-57-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-972-007-34

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Query Match          66.7%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      1 AAAA 4
        ||||
Db      1 AAAA 4

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RESULT 7

US-08-246-941-1

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; Sequence 1, Application US/08246941
; Patent No. 5543390
; GENERAL INFORMATION:
; APPLICANT: Yatvin, Milton. B.
; APPLICANT: Stowell, Michael H.B.
; APPLICANT: Gallicchio, Vincent S.
; APPLICANT: Meredith, Michael J.
; TITLE OF INVENTION: Covalent Microparticle-Drug Conjugates
; TITLE OF INVENTION: For Biological Targeting
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegratti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA

```

```

;      ZIP: 60606
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.25
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/246,941
;      FILING DATE: 19-MAY-1994
;      CLASSIFICATION: 514
;      ATTORNEY/AGENT INFORMATION:
;      NAME: No. 5543390nan, Kevin E
;      REGISTRATION NUMBER: 35,303
;      REFERENCE/DOCKET NUMBER: 90,663-M
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 312-715-1000
;      TELEFAX: 312-715-1234
;      TELEX: 910-221-5317
;      INFORMATION FOR SEQ ID NO: 1:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 4 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: peptide
;      FEATURE:
;      NAME/KEY: Modified-site
;      LOCATION: 1..4
;      OTHER INFORMATION: /label= multimer
;      OTHER INFORMATION: /note= "The peptide comprises whole-integer
;      OTHER INFORMATION: multiples of the basic sequence, having a total
;      OTHER INFORMATION: length of 4-20 Ala residues"
US-08-246-941-1

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Query Match          66.7%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      1 AAAA 4
        ||||
Db      1 AAAA 4

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RESULT 8

US-08-351-058A-2

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; Sequence 2, Application US/08351058A
; Patent No. 5550215
; GENERAL INFORMATION:
; APPLICANT: Holmes, Christopher P.
; TITLE OF INVENTION: Polymer Reversal on Solid Surfaces
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-1404

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/351,058A
; FILING DATE: 28-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,940
; FILING DATE: 19-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,727
; FILING DATE: 22-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-351-058A-2

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Query Match          66.7%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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```

Qy      1 AAAA 4
        ||||
Db      1 AAAA 4

```

RESULT 9

US-08-282-860-1

```

; Sequence 1, Application US/08282860
; Patent No. 5561108
; GENERAL INFORMATION:
; APPLICANT: Tsay, Grace C.
; APPLICANT: Cheung, Neal K. H.
; APPLICANT: Bettencourt, Jeffrey D.
; TITLE OF INVENTION: Preparation of Alpha-1 Antichymotrypsin
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 800 Dwight Way
; STREET: P. O. Box 1986
; CITY: Berkeley
; STATE: California
; COUNTRY: USA

```

```

;      ZIP: 94701-1986
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb Storage
;      COMPUTER: IBM
;      OPERATING SYSTEM: DOS
;      SOFTWARE: WordPerfect 6.1
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/282,860
;      FILING DATE: 07/29/94
;      CLASSIFICATION: 514
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Giblin, James A.
;      REGISTRATION NUMBER: 25772
;      REFERENCE/DOCKET NUMBER: MSB-7214
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (510)705-7910
;      TELEFAX: (510)705-7904
;      INFORMATION FOR SEQ ID NO: 1:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 4
;      TYPE: amino acid
;      STRANDEDNESS: single strand
;      TOPOLOGY: linear
;      MOLECULE TYPE:
;      DESCRIPTION: peptide
;      FEATURE:
;      NAME/KEY: Modified peptide used for enzyme activity assay
;      OTHER INFORMATION: Peptide is modified with n-terminal
;      OTHER INFORMATION: succinyl group and c-terminal p-nitroanilide group
;      PUBLICATION INFORMATION:
;      AUTHORS: Del Mar, E. G.
;      AUTHORS: Largman, C.
;      AUTHORS: Broderick, J. W.
;      TITLE: A Sensitive New Substrate for Chymotrypsin
;      JOURNAL: Analytical Biochemistry
;      VOLUME: 99
;      PAGES: 316-329
;      DATE: 01-NOV-1979
;      RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 4
US-08-282-860-1

```

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Query Match          66.7%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches    4; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy      . 3 AAPF 6
        ||||
Db      1 AAPF 4

```

```

RESULT 10
US-08-407-000-6
; Sequence 6, Application US/08407000
; Patent No. 5578324

```

```

; GENERAL INFORMATION:
; APPLICANT: Dohi, Masahiko
; APPLICANT: Nishibe, Yoshihisa
; APPLICANT: Makino, Yuji
; APPLICANT: Suzuki, Yoshiki
; TITLE OF INVENTION: PEPTIDE PROTEINACEOUS DRUG NASAL
; TITLE OF INVENTION: POWDER COMPOSITION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/407,000
; FILING DATE: 29-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/01257
; FILING DATE: 29-JUL-1994
; APPLICATION NUMBER: JP-A-5-206922
; FILING DATE: 30-JUL-1993
; APPLICATION NUMBER: JP-A-5-235841
; FILING DATE: 30-AUG-1993
; APPLICATION NUMBER: JP-A-6-1644
; FILING DATE: 12-JAN-1994
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-407-000-6

```

```

Query Match          66.7%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      3 AAPF 6
        ||||
Db      1 AAPF 4

```

```

RESULT 11
US-07-890-422B-28
; Sequence 28, Application US/07890422B
; Patent No. 5602102
; GENERAL INFORMATION:
; APPLICANT: THIELE, DWAIN L.
; APPLICANT: LIPSKY, PETER E.
; APPLICANT: MCGUIRE, MICHAEL J.

```

```

; TITLE OF INVENTION: DIPEPTIDYL PEPTIDASE-I
; TITLE OF INVENTION: INHIBITORS AND USES THEREOF
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/890,422B
; FILING DATE: 19920529
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MAYFIELD, DENISE L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: UTSD:296/MAY
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-320-7200
; TELEFAX: 512-474-7577
; TELEX: NOT APPLICABLE
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acid residues
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-890-422B-28

```

```

Query Match          66.7%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      3 AAPF 6
        ||||
Db      1 AAPF 4

```

RESULT 12

US-08-276-936A-2

; Sequence 2, Application US/08276936A

; Patent No. 5612194

; GENERAL INFORMATION:

; APPLICANT: Harvey Rubin, Barry Cooperman, No. 5612194man Schecter,

; APPLICANT: Michael Plotkin, Zhi Wang

; TITLE OF INVENTION: Methods of Producing Effective

; TITLE OF INVENTION: Recombinant Serine Protease Inhibitors and Uses of
These

; TITLE OF INVENTION: Inhibitors

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jane Massey Licata, Esq.

```

; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,936A
; FILING DATE: July 19, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 221,078
; FILING DATE: March 31, 1994
; APPLICATION NUMBER: 221,171
; FILING DATE: March 31, 1994
; APPLICATION NUMBER: 005,908
; FILING DATE: January 15, 1993
; APPLICATION NUMBER: 735,335
; FILING DATE: July 24, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: PENN-0027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-276-936A-2

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Query Match          66.7%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      3 AAPF 6
        ||||
Db      1 AAPF 4

```

```

RESULT 13
US-08-345-820B-2
; Sequence 2, Application US/08345820B
; Patent No. 5618792
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SUBSTITUTED HETEROCYCLIC COMPOUNDS USEFUL AS
; TITLE OF INVENTION: INHIBITORS OF (SERINE PROTEASES) HUMAN NEUTROPHIL
ELASTASE
; NUMBER OF SEQUENCES: 4
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/345,820B
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-345-820B-2

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Query Match          66.7%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      3 AAPF 6
        ||||
Db      1 AAPF 4

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RESULT 14

US-08-544-143A-3

```

; Sequence 3, Application US/08544143A
; Patent No. 5646028
; GENERAL INFORMATION:
; APPLICANT: Leigh, Scott D.
; TITLE OF INVENTION: NOVEL ALKALINE PROTEASE AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111-4121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/544,143A
; FILING DATE: 17-OCT-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: de Runtz, K. Alison
; REGISTRATION NUMBER: 37,119
; REFERENCE/DOCKET NUMBER: 0409.054US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-362-5556
; TELEFAX: 415-362-5418
; INFORMATION FOR SEQ ID NO: 3:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-544-143A-3

Query Match 66.7%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AAPF 6
|||
Db 1 AAPF 4

RESULT 15

US-08-397-602A-9

; Sequence 9, Application US/08397602A
; Patent No. 5646044
; GENERAL INFORMATION:
; APPLICANT: Wilson, Charles R
; APPLICANT: Tang, Maria R
; APPLICANT: Berger, Harald
; APPLICANT: Christianson, Teresa M
; APPLICANT: Hansen, Dieter
; TITLE OF INVENTION: Expression Systems for the Production
; TITLE OF INVENTION: of Target Proteins in Bacillus
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henkel Corporation Law Department
; STREET: 140 Germantown Pike, Suite 150
; CITY: Plymouth Meeting
; STATE: PA
; COUNTRY: USA
; ZIP: 19462
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,602A
; FILING DATE: 02-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jaeschke, Wayne C
; REGISTRATION NUMBER: 21,062
; REFERENCE/DOCKET NUMBER: D8969/M4828
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 832-2200
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

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;      TOPOLOGY:  linear
;      MOLECULE TYPE:  peptide
;      FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  1
;      OTHER INFORMATION:  /note= "N-SUCCINYL"
;      FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  4
;      OTHER INFORMATION:  /note=
;      OTHER INFORMATION:  "P-NITROANILIDE"
US-08-397-602A-9

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Best Local Similarity 100.0%;  Pred. No. 2.5e+05;
Matches      4;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

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Qy      3 AAPF 6
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Db      1 AAPF 4

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Job time : 16.8571 secs

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OM protein - protein search, using sw model

Run on: December 30, 2003, 12:16:11 ; Search time 42.8571 Seconds
(without alignments)
22.222 Million cell updates/sec

Title: US-10-033-526-4
Perfect score: 6
Sequence: 1 AAAAPF 6

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 50015

Minimum DB seq length: 4
Maximum DB seq length: 6

Post-processing: Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

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- 2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
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- 22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
- 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	6	100.0	6	23	AAO18046		C-terminal truncat
2	4	66.7	4	5	AAP40459		N-terminal polyhyd
3	4	66.7	4	11	AAR04012		Peptidase substrat
4	4	66.7	4	12	AAR10887		Peptide component
5	4	66.7	4	12	AAR11223		Ketone analogue pr
6	4	66.7	4	13	AAR26239		Alpha-keto peptide
7	4	66.7	4	13	AAR26243		Peptide keto ester
8	4	66.7	4	13	AAR29964		Cathepsin G inhibi
9	4	66.7	4	14	AAR34258		Chromogenic peptid
10	4	66.7	4	14	AAR38410		Cathepsin G inhibi
11	4	66.7	4	14	AAR44109		Aminonaphthalene p
12	4	66.7	4	15	AAR52024		Bacillus alkali pr
13	4	66.7	4	15	AAR47854		Calpain inhibitor.
14	4	66.7	4	15	AAR46223		Serine protease in
15	4	66.7	4	15	AAR53781		Sequence of intern
16	4	66.7	4	16	AAR72920		Substrate for pept
17	4	66.7	4	16	AAR72876		Substrate for pept
18	4	66.7	4	16	AAR64756		RDA linking group.
19	4	66.7	4	16	AAR64757		RDA linking group.
20	4	66.7	4	16	AAR64758		RDA linking group.
21	4	66.7	4	16	AAR64759		RDA linking group.
22	4	66.7	4	16	AAR64760		RDA linking group.
23	4	66.7	4	16	AAR64761		RDA linking group.
24	4	66.7	4	16	AAR77315		Porphyromonas ging
25	4	66.7	4	16	AAR77196		Cell proliferation
26	4	66.7	4	17	AAR85709		Degradable peptide
27	4	66.7	4	18	AAW52606		Serine protease-in
28	4	66.7	4	18	AAW34656		Mutated peptide de
29	4	66.7	4	18	AAW29405		Elastase inhibitor
30	4	66.7	4	18	AAW30747		Substrate peptide
31	4	66.7	4	18	AAW24567		Substrate for seri
32	4	66.7	4	18	AAW08165		Proteinase site of
33	4	66.7	4	18	AAW12810		Synthetic substrat
34	4	66.7	4	19	AAW79700		B. subtilis subtil
35	4	66.7	4	19	AAW76694		B. subtilis subtil
36	4	66.7	4	19	AAW61357		Synthetic oligopep
37	4	66.7	4	19	AAW51451		Indicator for dete
38	4	66.7	4	19	AAW51610		Peptide conjugated
39	4	66.7	4	19	AAW59262		BOP activated pept
40	4	66.7	4	20	AAM48424		Alkaline protease-
41	4	66.7	4	20	ABB07072		Alkaline protease
42	4	66.7	4	20	AAY50256		Neutrophil-activat
43	4	66.7	4	20	AAW84189		Peptide comprising
44	4	66.7	4	21	AAB20774		Chymotrypsin enzym
45	4	66.7	4	21	AAB03092		Substrate peptide

ALIGNMENTS

RESULT 1

AAO18046

ID AAO18046 standard; peptide; 6 AA.

XX

AC AAO18046;

XX

DT 30-AUG-2002 (first entry)

XX

DE C-terminal truncated apoE formation inhibitor peptide #4.

XX

KW C-terminal truncated apoE; apolipoprotein E; apoE; Alzheimer's disease;

KW neurofibrillary tangle; apoE4 allele; nootropic; neuroprotective;

KW cardiant; vulnerary; cerebroprotective; coronary artery disease;

KW head trauma; stroke.

XX

OS Synthetic.

XX

PN WO200238108-A2.

XX

PD 16-MAY-2002.

XX

PF 02-NOV-2001; 2001WO-US51172.

XX

PR 03-NOV-2000; 2000US-245737P.

XX

PA (GLAD-) GLADSTONE INST J DAVID.

XX

PI Huang Y, Mahley RW;

XX

DR WPI; 2002-490051/52.

XX

PT Inhibiting neurofibrillary tangles formation, useful for treating e.g.

PT Alzheimer's, coronary artery disease or stroke, by reducing the

PT formation of carboxyl-terminal truncated form of apolipoprotein E in a

PT neuron of the individual -

XX

PS Claim 24; Page 62; 75pp; English.

XX

CC The present invention relates to a method of inhibiting the formation of

CC neurofibrillary tangles in an individual, which involves reducing the

CC formation of a carboxyl-terminal truncated form of apolipoprotein E

CC (apoE) in a neurone in the individual. The method is useful for

CC inhibiting the formation of neurofibrillary tangles in an individual. The

CC reduction in the formation of carboxyl-terminal truncated apoE treats a

CC disorder related to apoE in an individual, specifically Alzheimer's

CC disease, coronary artery disease, head trauma or stroke. The present

CC sequence is a peptide capable of inhibiting the formation of the

CC C-terminal truncated form of apoE.

XX

SQ Sequence 6 AA;

Query Match 100.0%; Score 6; DB 23; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAPF 6
| | | | |

Db

1 AAAAPF 6

RESULT 2

AAP40459

ID AAP40459 standard; Protein; 4 AA.

XX

AC AAP40459;

XX

DT 25-MAR-2003 (updated)

DT 09-JAN-2003 (updated)

DT 27-NOV-1991 (first entry)

XX

DE N-terminal polyhydroxyalkanoyl peptide.

XX

KW Polyhydroxyalkanoyl peptide; protease; peptidase; prodrug.

XX

OS Unidentified.

XX

PN EP126685-A.

XX

PD 28-NOV-1984.

XX

PF 15-MAY-1984; 84EP-0400984.

XX

PR 16-MAY-1983; 83FR-0008051.

XX

PA (CNRS) CENT NAT RECH SCI.

XX

PI Monsigny M, Mayer R;

XX

DR WPI; 1984-296065/48.

XX

PT N-terminal polyhydroxyalkanoyl peptide and aminoacid derivs. - opt.
PT having C-terminal active gps., e.g. chloroquine, are water-soluble
PT antitumour or antiparasitic cpds. and protease targets.

XX

PS Claim 11; page 15; 20pp; french.

XX

CC The peptide is polyhydroxyalkanoyl-L-Ala-L-Ala-L-Pro-L-Phe-X. X is
CC R2-NH- derived from an aromatic amine, eg P-nitro-aniline, alpha-
CC or beta-naphthylamine, or it is R3NH derived from an amino drug, eg
CC daunorubicin or chloroquine, or it is a gp. which may confer
CC activity, eh H, OH, CH2Cl. When X is the residue of a drug, the
CC cpd. is a prodrug in which the peptide is the substrate for a
CC specific protease secreted by the target cell for the active drug,
CC eg tumour cells or microorganism pathogens, eg Plasmodium
CC falciparum. Due to the polyhydroxy gp., the cpds. are very soluble
CC in water or buffer soln. and are able to be used at high concn. The
CC cpds. also allow the detection of proteases and peptidases and
CC allow easy determination of the best substrate for a particular
CC protease.

CC (Updated on 09-JAN-2003 to add missing OS field.)

CC (Updated on 25-MAR-2003 to correct PD field.)

CC (Updated on 25-MAR-2003 to correct PR field.)

CC (Updated on 25-MAR-2003 to correct PA field.)

XX

SQ Sequence 4 AA;

Query Match 66.7%; Score 4; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AAPF 6
 ||||
Db 1 AAPF 4

RESULT 3

AAR04012

ID AAR04012 standard; peptide; 4 AA.

XX

AC AAR04012;

XX

DT 25-MAR-2003 (updated)

DT 19-NOV-1991 (first entry)

XX

DE Peptidase substrate analogues having peptidase inhibition activity.

XX

KW Elastase; plasminogen activator; cathepsin; calpain; enkephalinase;

KW Angiotensin converting enzyme.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 4

FT /label= Terminal modified from -COOH to -COCOR

FT /note= "R = alkyl group or -H"

XX

PN EP363284-A.

XX

PD 11-APR-1990.

XX

PF 06-OCT-1989; 89EP-0402762.

XX

PR 07-OCT-1988; 88US-0254762.

PR 06-OCT-1989; 89EP-0402763.

XX

PA (RICH) MERRELL DOW PHARM INC.

PA (RICH) MERRELL PHARM INC.

XX

PI Bey P, Angelastro M, Mehdi S;

XX

DR WPI; 1990-109579/15.

XX

PT New peptidase substrate analogue cpds. - useful as protease
PT inhibitors in treatment of disease states.

XX

PS Claim 5; Page 26; 33pp; English.

XX

CC The analogues may be useful in treatment of a variety of disease
CC states. The scissile amide group is replaced with H or a substituted
CC Carbon moiety effectively inhibiting the activity of peptidases such
CC as elastase, plasmin thrombin, urokinase etc.

CC (Updated on 25-MAR-2003 to correct PA field.)

XX

SQ Sequence 4 AA;

Query Match 66.7%; Score 4; DB 11; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AAPF 6

||||

Db 1 AAPF 4

RESULT 4

AAR10887

ID AAR10887 standard; Protein; 4 AA.

XX

AC AAR10887;

XX

DT 10-APR-1991 (first entry)

XX

DE Peptide component of pentafluoroethylcarbonyl analogue.

XX

KW Protease inhibitor; rheumatoid arthritis; thrombosis; psoriasis;
KW male contraceptive.

XX

OS Synthetic.

XX

PN EP410411-A.

XX

PD 30-JAN-1991.

XX

PF 25-JUL-1990; 90EP-0114250.

XX

PR 26-JUL-1989; 89US-0385624.

XX

PA (RICH) MERRELL DOW PHARM INC.

XX

PI Bey P, Peet NP, Angelastro MR, Mehdi S;

XX

DR WPI; 1991-030811/05.

XX

PT Novel serine-, carboxylic acid-and metallo-proteinase-inhibitors

PT - inhibit range of proteinase(s) in treating rheumatoid

PT arthritis, thrombosis and psoriasis, also is a male contraceptive

XX

PS Claim 5; page 25; 40pp; English.

XX

CC This peptide is the R1 gp. of the cpd. of formula: R1NHCH(R2)-
CC COCF2CF3. This cpd. is a peptidase substrate analogue and is a
CC specific enzyme inhibitor for a range of proteases, e.g. serine-,
CC carboxylic acid-, and metallo-proteases. It is useful in the
CC treatment of rheumatoid arthritis, thrombosis and psoriasis and is
CC also used as a male contraceptive. See also AAR10876-83, AAR10886 and
CC AAR10888.

XX

SQ Sequence 4 AA;

Query Match 66.7%; Score 4; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AAPF 6
 |||
Db 1 AAPF 4

RESULT 5

AAR11223

ID AAR11223 standard; Protein; 4 AA.

XX

AC AAR11223;

XX

DT 24-MAY-1991 (first entry)

XX

DE Ketone analogue protease inhibitor #2.

XX

KW protease inhibitor; antiinflammatory agent; hypotensive; analgesic;

KW antiproliferative agent; antidemyelinating agent; antithrombotic.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /label= Methoxysuccinyl-Ala

FT Modified-site 4

FT /label= Phe-carboxyoxalyl

XX

PN EP417721-A.

XX

PD 20-MAR-1991.

XX

PF 11-SEP-1990; 90EP-0117461.

XX

PR 11-SEP-1989; 89US-0405491.

XX

PA (RICH) MERRELL DOW PHARM INC.

XX

PI Flynn GA, Bey P;

XX

DR WPI; 1991-081980/12.

XX

PT New ketone analogue peptidase and isomerase inhibitors - for

PT inhibition of leukocyte elastase, cathepsin G, thrombin,

PT chymotrypsin, plasmin etc.

XX

PS Claim 5; Page 26; 50pp; English.

XX

CC This peptide is a specific example of a highly generic protease

CC inhibitor useful for medical purposes. The peptide analogues include

CC inhibitors of urokinase, renin, cathepsin D, etc. which can be used

CC as anti-proliferative agents and abortifacients, hypotensives,

CC antiinflammatory and antidemyelinating agents, respectively.

CC See also AAR11222 and AAR11224-R11238.

XX

SQ Sequence 4 AA;

Query Match 66.7%; Score 4; DB 12; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AAPF 6

||||

Db 1 AAPF 4

RESULT 6

AAR26239

ID AAR26239 standard; peptide; 4 AA.

XX

AC AAR26239;

XX

DT 25-MAR-2003 (updated)

DT 27-JAN-1993 (first entry)

XX

DE Alpha-keto peptide protease inhibitors.

XX

KW serine protease inhibitor; cysteine protease inhibitor; chymase;

KW chymotrypsin; elastase; trypsin; blood coagulation enzyme;

KW antiinflammatory; anticoagulant; neuroprotectant; emphysema; ARDS;

KW arthritis; ischaemia; stroke; Alzheimer's disease; tumour;

KW metastases; bone resorption.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Z-Ala"

FT Modified-site 4

FT /note= "keto-ester DL-Ala-COOEt"

XX

PN W09212140-A1.

XX

PD 23-JUL-1992.

XX

PF 27-DEC-1991; 91WO-US09801.

XX

PR 28-DEC-1990; 90US-0635287.

XX

PA (GEOR-) GEORGIA TECH RES CORP.

XX

PI Powers JC;

XX

DR WPI; 1992-268589/32.

XX

PT New alpha-keto:amide, alpha-keto:acid and alpha-keto:ester

PT derivs. - inhibit serine and cysteine protease(s) and are used

PT for treating and preventing inflammation, emphysema, adult

PT respiratory distress syndrome, etc.

XX

PS Example 6; Page 42; 88pp; English.

XX
 CC The peptide is one example of a highly generic group of amino acids
 CC and di-, tri- and tetra-peptides having alpha-keto functionality at
 CC the C-terminal, the compounds optionally being in amide or ester form.
 CC These compounds are selective or general inhibitors of serine and
 CC cysteine proteases, e.g. chymases, chymotrypsin-like enzymes,
 CC elastases, trypsin, and blood coagulation enzymes. They are useful
 CC as antiinflammatory agents, anticoagulants, neuroprotectants and for
 CC treatment of neurodegeneration in cases of e.g. emphysema, ARDS,
 CC arthritis, ischaemia, stroke, Alzheimer's disease, tumour metastases
 CC and bone resorption. They are also useful in-vitro for protecting
 CC sensitive materials against proteolysis.
 CC The present compound is specifically an elastase inhibitor.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 4 AA;

Query Match 66.7%; Score 4; DB 13; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAA 4
 ||||
 Db 1 AAAA 4

RESULT 7

AAR26243

ID AAR26243 standard; peptide; 4 AA.

XX

AC AAR26243;

XX

DT 25-MAR-2003 (updated)

DT 28-JAN-1993 (first entry)

XX

DE Peptide keto esters for treating neurodegeneration.

XX

KW Calpain inhibitor; HIV; excitotoxicity; ischaemia; haemorrhage;
 KW stroke; dementia; Alzheimer; Huntington; chorea; Parkinson; carbon;
 KW monoxide poisoning; drowning; brain injury.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Z-Ala"

FT Modified-site 4

FT /note= "DL-Ala-COOEt (i.e. keto ester)"

XX

PN WO9211850-A1.

XX

PD 23-JUL-1992.

XX

PF 27-DEC-1991; 91WO-US09786.

XX

PR 28-DEC-1990; 90US-0635952.

XX

PA (CORT-) CORTEX PHARM INC.
 PA (GEOR-) GEORGIA TECH RES CORP.
 XX
 PI Bartus RT, Eveleth DD, Lynch GS, Powers JC;
 XX
 DR WPI; 1992-268380/32.
 XX
 PT Treatment of neuro-degeneration using Calpain inhibitors - e.g.
 PT substd. iso-coumarin(s), peptide keto-compounds and halo-ketone
 PT peptide(s)
 XX
 PS Claims 51,71; Pages 120,122; 132pp; English.
 XX
 CC The peptide is one example of calpain inhibitors claimed for use in
 CC treatment of neurodegeneration due to excitotoxicity, HIV-induced
 CC neuropathy, ischaemia, subarachnoid haemorrhage, stroke, multiple
 CC infarction dementia, Alzheimer's disease, Huntington's chorea,
 CC Parkinson's disease, etc., or due to ischaemia-inducing events such
 CC as head injury, major heart attack, brain seizure, near drowning,
 CC carbon monoxide poisoning or surgery-related brain damage.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 4 AA;

Query Match 66.7%; Score 4; DB 13; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAA 4
 ||||
 Db 1 AAAA 4

RESULT 8

AAR29964

ID AAR29964 standard; peptide; 4 AA.

XX

AC AAR29964;

XX

DT 25-MAR-2003 (updated)

DT 19-APR-1993 (first entry)

XX

DE Cathepsin G inhibiting fragment.

XX

KW Cathepsin G; elastase; connective tissue; degradation; protease;

KW gout; rheumatoid arthritis; emphysema; ARDS;

KW adult respiratory distress syndrome; para-phenylene.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal amino acids of the peptides of

FT AAR29963-64 are pref. linked by

FT -C(O)-phenylene-C(O)-, esp. wherein the

FT phenylene is a para-phenylene gp."

FT Modified-site 4

FT /note= "C-terminal Phe is in keto form, i.e. OH
 FT replaced by CGIM, pref. CF3 or CF2CF3"
 XX
 PN WO9220357-A1.
 XX
 PD 26-NOV-1992.
 XX
 PF 21-APR-1992; 92WO-US03288.
 XX
 PR 23-MAY-1991; 91US-0704499.
 XX
 PA (RICH) MERRELL DOW PHARM INC.
 XX
 PI Angelastro MR, Bey P, Doherty NS, Janusz MJ, Mehdi S;
 PI Peet NP;
 XX
 DR WPI; 1992-415461/50.
 XX
 PT New peptide derivs. used as cathepsin G and elastase inhibitors -
 PT for treating gout, rheumatoid arthritis, inflammatory disorders,
 PT emphysema and adult respiratory distress syndrome
 XX
 PS Claim 13-17; Page 52; 53pp; English.
 XX
 CC This sequence is an example of a highly generic formula.
 CC Inhibitors of cathepsin G and elastase for preventing connective
 CC tissue degradation are chemically linked inhibitors of the proteases
 CC elastase (pref. the peptide of AAR29963, or Lys(2CBz)-Pro-Val or
 CC Val-Pro-Val) and cathepsin G (pref. the peptide of AAR29964, or
 CC Val-Pro-Phe or Phe).
 CC The N-terminal amino acids of the peptides of AAR29963-64 are pref.
 CC linked by -C(O)-phenylene-C(O)-, esp. wherein the phenylene is a
 CC para-phenylene gp.
 CC The cpds. have an anti-inflammatory effect useful in the treatment
 CC of gout, rheumatoid arthritis and other inflammatory diseases and
 CC to prevent elastin mediated tissue damage. They can also be used
 CC in the treatment of emphysema and adult respiratory distress syndrome.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 4 AA;

 Query Match 66.7%; Score 4; DB 13; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 3 AAPF 6
 ||||
 Db 1 AAPF 4

RESULT 9
 AAR34258
 ID AAR34258 standard; peptide; 4 AA.
 XX
 AC AAR34258;
 XX

DT 25-MAR-2003 (updated)
 DT 19-AUG-1993 (first entry)
 XX
 DE Chromogenic peptide substrate for peptidase assay.
 XX
 KW Alkaline protease; detergent; stability.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-succinyl alanine"
 FT Modified-site 4
 FT /note= "Phe-p-nitroanilide"
 XX
 PN W09307276-A1.
 XX
 PD 15-APR-1993.
 XX
 PF 07-OCT-1992; 92WO-US08341.
 XX
 PR 08-OCT-1991; 91US-0772087.
 XX
 PA (CHEM-) CHEMGEN CORP.
 PA (VIST-) VISTA CHEMICAL CO.
 XX
 PI Fodge DW, Hsiao H, Lalonde JJ;
 XX
 DR WPI; 1993-134465/16.
 XX
 PT Alkaline protease produced by bacillus stable in alkaline
 PT conditions - used in detergents and bleaches to decompose
 PT proteinaceous stains
 XX
 PS Disclosure; Page 8; 58pp; English.
 XX
 CC The peptide is a chromogenic substrate for use in a peptidase assay
 CC to test the peptidase activity of a novel alkaline protease.
 CC Detergent was found to interfere with the assay by reducing the
 CC protease activity. See also AAR34259-61 and AAR34463-66.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 4 AA;

 Query Match 66.7%; Score 4; DB 14; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AAPF 6
 ||||
 Db 1 AAPF 4

RESULT 10
 AAR38410
 ID AAR38410 standard; Protein; 4 AA.
 XX

AC AAR38410;
XX
DT 29-OCT-1993 (first entry)
XX
DE Cathepsin G inhibitor peptide #1.
XX
KW Inflammatory disease; prevention; rheumatoid arthritis; emphysema;
KW neutrophil-mediated connective tissue degradation; gout; elastase;
KW inhibition; adult respiratory distress syndrome.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "Linked via a linking chain such as
FT -CO-phenylene-CO- to the N-terminal of a
FT Cathepsin G inhibiting molecule as described
FT in AAR38410-11"
FT Modified-site 4
FT /note= "May opt. be modified by COCOR, CF2CF3, CF3,
FT CHF2, COOR3, CONHR3, CF2CHR3CONHR, H, alkyl,
FT aryl, aralkyl or COR; where R3 is H, alkyl,
FT phenyl or benzyl and R is OH or alkoxy"
XX
PN ZA9203602-A.
XX
PD 24-FEB-1993.
XX
PF 18-MAY-1992; 92ZA-0003602.
XX
PR 23-MAY-1991; 91US-0704499.
XX
PA (RICH) MERRELL DOW PHARM INC.
XX
PI Angelastro MM, Bey P, Doherty NS, Janusz MJ, Mehdi S;
PI Peet NP;
XX
DR WPI; 1993-197380/24.
XX
PT New cathepsin G and elastase inhibitors - prevents connective
PT tissue degradation
XX
PS Claim 13-17; Page 52; 55pp; English.
XX
CC The sequences given in AAR38410-11 are cathepsin G inhibiting peptides
CC which were produced by standard peptide synthesis methods. In the
CC context of the invention one of these peptides may be linked via
CC their N-termini to an elastase inhibiting peptide (see features
CC table). The peptide conjugates may be used to prevent neutrophil-
CC mediated connective tissue degradation associated with inflammatory
CC diseases eg. gout and rheumatoid arthritis. They may also be used
CC for preventing elastin-mediated tissue damage in the treatment of
CC emphysema and adult respiratory distress syndrome.
XX
SQ Sequence 4 AA;

Query Match

66.7%; Score 4; DB 14; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAPF 6
 ||||
Db 1 AAPF 4

RESULT 11

AAR44109

ID AAR44109 standard; peptide; 4 AA.

XX

AC AAR44109;

XX

DT 25-MAR-2003 (updated)

DT 16-MAY-1994 (first entry)

XX

DE Aminonaphthalene propyl sulphamide tetrapeptide.

XX

KW chymotrypsin assay; ansa-substrate; detector group.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /label= OTHER

FT /note= "Suc-Ala (Claim 1) or Z-Ala (Claim 2)"

FT Modified-site 4

FT /label= OTHER

FT /note= "Phe-NH-(1,5-naphthylene)-SO₂NH-C₃H₇"

XX

PN SU1771478-A3.

XX

PD 23-OCT-1992.

XX

PF 20-JUL-1990; 90SU-4872552.

XX

PR 20-JUL-1990; 90SU-4872552.

XX

PA (ALIB=) AS LITH BIOCHEM INST.

PA (ASMO=) AS USSR MOLECULAR GENETICS.

XX

PI Nedospasov AA, Palaima AI, Yanchene RA;

XX

DR WPI; 1993-358242/45.

XX

PT Prepn. of new succinyl-alanyl-alanyl-propyl-phenylalanyl-amino-

PT naphthalen-propyl-sulphamide - for use as ansa-substrate in the

PT quantitative determn. of chymotrypsin

XX

PS Claim 1 and 2; Column 8; 4pp; Russian.

XX

CC 5-(N-succinyl-alanyl-alanyl-prolyl-phenylalanyl)aminonaphthalene-1-

CC (N-propyl)sulphamide (Claim 1) and 5-(N-benzyloxycarbonyl-alanyl-

CC alanyl-prolyl-phenylalanyl)aminonaphthalene-1-(N-propyl)sulphamide

CC (Claim 2) are prepared by initially reacting N-benzyloxycarbonyl-

CC phenylalanine with isobutyl chloroformate in tetrahydrofuran

CC followed by reaction with 5-aminonaphthalene-1-(N-propyl)sulphamide.
CC The new compounds are used as detector groups in quantitative
CC determination of chymotrypsin.
CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 4 AA;

Query Match 66.7%; Score 4; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AAPF 6

||||

Db 1 AAPF 4

RESULT 12

AAR52024

ID AAR52024 standard; peptide; 4 AA.

XX

AC AAR52024;

XX

DT 28-NOV-1994 (first entry)

XX

DE Bacillus alkali protease substrate.

XX

KW Bacillus NKS-21 alkali protease; hydrolysis; thermostable enzyme;

KW detergent stable.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /label= OTHER

FT /note= "Suc-Ala"

FT Modified-site 4

FT /label= OTHER

FT /note= "Phe-MCA"

XX

PN JP06070765-A.

XX

PD 15-MAR-1994.

XX

PF 08-OCT-1992; 92JP-0296360.

XX

PR 10-JUL-1992; 92JP-0207302.

XX

PA (SHOW) SHOWA DENKO KK.

XX

DR WPI; 1994-128672/16.

XX

PT New alkali protease stable to heat and detergent - useful as

PT industrial enzyme, eg in washing compositions

XX

PS Claim 1; Page 2; 10pp; Japanese.

XX

CC A novel alkali protease obtained from Bacillus NKS-21 is defined by

CC its physico-chemical properties including substrate specificity for
CC the tetrapeptide AAR52024.

XX

SQ Sequence 4 AA;

Query Match 66.7%; Score 4; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AAPF 6

||||

Db 1 AAPF 4

RESULT 13

AAR47854

ID AAR47854 standard; peptide; 4 AA.

XX

AC AAR47854;

XX

DT 25-MAR-2003 (updated)

DT 22-JUN-1994 (first entry)

XX

DE Calpain inhibitor.

XX

KW Cell reproduction; dividing cells; G1 stage; chemotherapy; cancer;
KW neurodegeneration; Alzheimer's disease; ischaemia; subarachnoid;
KW haemorrhage.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "acylated"

FT Modified-site 4

FT /note= "Ala-CH2Cl"

XX

PN WO9400095-A2.

XX

PD 06-JAN-1994.

XX

PF 24-JUN-1993; 93WO-US06143.

XX

PR 24-JUN-1992; 92US-0903800.

PR 16-MAR-1993; 93US-0034996.

PR 01-JUN-1993; 93US-0072609.

XX

PA (CORT-) CORTEX PHARM INC.

PA (GEOR-) GEORGIA TECH RES CORP.

XX

PI Bartus RT, Eveleth DD, Lynch G, Powers JC;

XX

DR WPI; 1994-025846/03.

XX

PT Blocking actively dividing cells in G1 stage using calpain
PT inhibitor - esp. to increase efficiency of cancer chemotherapy
PT and cell transformation, inhibitors also useful for treating e.g.

PT muscle damage, cataract, vasospasm etc.

XX

PS Example 1C; Page 163; 258pp; English.

XX

CC The compound is an example of a calpain inhibitor which may be used
CC to synchronise the reproductive cycle in actively reproducing cells,
CC by blocking cell progression from the G1 to S phase. This
CC synchronisation is used to shorten the duration of chemotherapy of
CC cancer and to increase activity of the chemotherapeutic agent and to
CC increase the efficiency of cell transformation or integration of
CC foreign DNA into cells. Activation by calpain is an early event
CC leading to cell death and damage, so the cpd. may be used to treat
CC such cells before extensive damage occurs, e.g. to treat
CC neurodegeneration in ischaemia, subarachnoid haemorrhage and
CC Alzheimer's disease.

CC AAR47852-3.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 4 AA;

Query Match 66.7%; Score 4; DB 15; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAA 4

||||

Db 1 AAAA 4

RESULT 14

AAR46223

ID AAR46223 standard; peptide; 4 AA.

XX

AC AAR46223;

XX

DT 04-AUG-1994 (first entry)

XX

DE Serine protease inhibitor tetrapeptide.

XX

KW Prevention; schistosomiasis; parasite; infection; prevention;
KW parasitic penetration; skin; cercariae; anti-penetrant.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "BG(peptide blocking gp.) attached"

FT Modified-site 4

FT /note= "PI(protease inhibitor), other than
FT chloromethyl ketone, attached"

XX

PN US5284829-A.

XX

PD 08-FEB-1994.

XX

PF 26-NOV-1991; 91US-0798565.

XX

PR 26-NOV-1991; 91US-0798565.

XX

PA (REGC) UNIV CALIFORNIA.

XX

PI Cohen FE, McKerrow JH;

XX

DR WPI; 1994-056364/07.

XX

PT Synthetic tetra:peptide(s) with an N-terminal blocking gp. and
PT C-terminal enzyme inhibitor - can be formulated into soaps and
PT sprays and used to prevent schistosomal skin penetration

XX

PS Disclosure; Page 7; 35pp; English.

XX

CC The sequence is that of a synthetic tetrapeptide serine protease
CC inhibitor which can be used to prevent schistosome parasite
CC infection. It may be used in a formulation as a soap, lotion,
CC cream, spray, etc. to stop parasitic penetration of the skin.

XX

SQ Sequence 4 AA;

Query Match 66.7%; Score 4; DB 15; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAPF 6

||||

Db 1 AAPF 4

RESULT 15

AAR53781

ID AAR53781 standard; Peptide; 4 AA.

XX

AC AAR53781;

XX

DT 25-MAR-2003 (updated)

DT 29-DEC-1994 (first entry)

XX

DE Sequence of internal fragment of a chromogenic substrate for
DE cathepsin G.

XX

KW Enzyme; cathepsin G; protease; chromogenic substrate.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /label= Suc-Ala

FT /note= "Succinyl group"

FT Modified-site 4

FT /label= Phe-pNA

FT /note= "p-nitroanil"

XX

PN W09412637-A2.

XX

PD 09-JUN-1994.

XX
 PF 01-DEC-1993; 93WO-US11696.
 XX
 PR 02-DEC-1992; 92US-0985692.
 PR 19-NOV-1993; 93US-0155331.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Foster DC, Norris K, Sprecher CA;
 XX
 DR WPI; 1994-200265/24.
 XX
 PT New human Kunitz type protease inhibitor and related DNA - for
 PT treating pancreatitis and other disorders involving serine
 PT protease, also new amyloid protein precursor homologues including
 PT the inhibitor in its sequence
 XX
 PS Example; Page 63; 70pp; English.
 XX
 CC Protease inhibitory profiles of the Kunitz inhibitors
 CC were determined for a variety of proteases using
 CC a variety of chromogenic substrates and compared to the inhibitory
 CC activity shown by the Kunitz-type inhibitor domain of the amyloid
 CC protein precursor and bovine aprotinin. The substrate AAR53780
 CC was tested using the protease leukocyte elastase.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 4 AA;

 Query Match 66.7%; Score 4; DB 15; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 3 AAPF 6
 ||||
 Db 1 AAPF 4

Search completed: December 30, 2003, 12:23:06
 Job time : 42.8571 secs

OM protein - protein search, using sw model

Run on: December 30, 2003, 12:23:47 ; Search time 30.4286 Seconds
(without alignments)
39.243 Million cell updates/sec

Title: US-10-033-526-4
Perfect score: 6
Sequence: 1 AAAAPF 6

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 724715 seqs, 199017464 residues

Word size : 0

Total number of hits satisfying chosen parameters: 18921

Minimum DB seq length: 4

Maximum DB seq length: 6

Post-processing: Listing first 45 summaries

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- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Length	DB	ID	Description
No.		%				
		Query				

1	6	100.0	6	14	US-10-033-526-4	Sequence 4, Appli
2	4	66.7	4	9	US-09-757-908A-15	Sequence 15, Appl
3	4	66.7	4	10	US-09-117-380B-2	Sequence 2, Appli
4	4	66.7	4	10	US-09-935-744-1	Sequence 1, Appli
5	4	66.7	4	12	US-10-373-794-3	Sequence 3, Appli
6	4	66.7	4	12	US-10-087-942-32	Sequence 32, Appl
7	4	66.7	4	12	US-10-443-701-2	Sequence 2, Appli
8	4	66.7	4	12	US-10-138-375-77	Sequence 77, Appl
9	4	66.7	4	12	US-10-397-160-66	Sequence 66, Appl
10	4	66.7	4	14	US-10-090-624-33	Sequence 33, Appl
11	4	66.7	4	14	US-10-036-371-7	Sequence 7, Appli
12	4	66.7	4	14	US-10-040-655-10	Sequence 10, Appl
13	4	66.7	4	14	US-10-033-526-1	Sequence 1, Appli
14	4	66.7	4	14	US-10-133-912-21	Sequence 21, Appl
15	4	66.7	4	14	US-10-041-006A-10	Sequence 10, Appl
16	4	66.7	4	15	US-10-087-905-32	Sequence 32, Appl
17	4	66.7	4	15	US-10-209-812-6	Sequence 6, Appli
18	4	66.7	4	15	US-10-155-886-32	Sequence 32, Appl
19	4	66.7	4	15	US-10-222-455-34	Sequence 34, Appl
20	4	66.7	4	15	US-10-104-693-6	Sequence 6, Appli
21	4	66.7	4	15	US-10-229-346-35	Sequence 35, Appl
22	4	66.7	5	9	US-09-040-518-9	Sequence 9, Appli
23	4	66.7	5	9	US-09-972-475-35	Sequence 35, Appl
24	4	66.7	6	9	US-09-802-077-36	Sequence 36, Appl
25	4	66.7	6	9	US-09-802-096-36	Sequence 36, Appl
26	4	66.7	6	10	US-09-994-927-1	Sequence 1, Appli
27	4	66.7	6	11	US-09-925-179-36	Sequence 36, Appl
28	4	66.7	6	14	US-10-099-895-43	Sequence 43, Appl
29	4	66.7	6	14	US-10-215-297-18	Sequence 18, Appl
30	4	66.7	6	15	US-10-215-298-18	Sequence 18, Appl
31	3	50.0	4	9	US-09-842-543-1	Sequence 1, Appli
32	3	50.0	4	9	US-09-757-908A-14	Sequence 14, Appl
33	3	50.0	4	10	US-09-202-077-12	Sequence 12, Appl
34	3	50.0	4	10	US-09-117-380B-1	Sequence 1, Appli
35	3	50.0	4	10	US-09-935-744-2	Sequence 2, Appli
36	3	50.0	4	11	US-09-928-117-1	Sequence 1, Appli
37	3	50.0	4	11	US-09-876-904A-19	Sequence 19, Appl
38	3	50.0	4	12	US-10-373-794-2	Sequence 2, Appli
39	3	50.0	4	12	US-10-087-942-33	Sequence 33, Appl
40	3	50.0	4	12	US-10-087-942-36	Sequence 36, Appl
41	3	50.0	4	12	US-10-354-706-1	Sequence 1, Appli
42	3	50.0	4	12	US-10-350-470-10	Sequence 10, Appl
43	3	50.0	4	12	US-10-125-222-1	Sequence 1, Appli
44	3	50.0	4	12	US-10-259-609-29	Sequence 29, Appl
45	3	50.0	4	12	US-10-352-786-63	Sequence 63, Appl

ALIGNMENTS

RESULT 1
 US-10-033-526-4
 ; Sequence 4, Application US/10033526
 ; Publication No. US20020147999A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert W. Mahley


```

; APPLICANT: Yadong Huang
; TITLE OF INVENTION: Methods of Treating Disorders Related to
; TITLE OF INVENTION: APOE
; FILE REFERENCE: UCAL217
; CURRENT APPLICATION NUMBER: US/10/033,526
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 60/245,737
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-033-526-4

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```

Query Match          100.0%; Score 6; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches      6; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      1 AAAAPF 6
        |||||
Db      1 AAAAPF 6

```

RESULT 2

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US-09-757-908A-15
; Sequence 15, Application US/09757908A
; Patent No. US20020052468A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell
; TITLE OF INVENTION: Disulfide Core Polypeptides
; FILE REFERENCE: 98-13D1
; CURRENT APPLICATION NUMBER: US/09/757,908A
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 09/326,039
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: US 60/088,136
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-757-908A-15

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Query Match          66.7%; Score 4; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches      4; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      3 AAPF 6
        |||
Db      1 AAPF 4

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RESULT 3

US-09-117-380B-2

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; Sequence 2, Application US/09117380B
; Patent No. US20020119917A1
; GENERAL INFORMATION:
; APPLICANT: FRIDKIN, Matityahu
; APPLICANT: YAVIN, Eran J.
; TITLE OF INVENTION: ANTI-INFLAMMATORY PEPTIDES DERIVED FROM C-REACTIVE
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: FRIDKIN=1
; CURRENT APPLICATION NUMBER: US/09/117,380B
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: PCT/IL97/00032
; PRIOR FILING DATE: 1997-01-27
; PRIOR APPLICATION NUMBER: IL 116976
; PRIOR FILING DATE: 1996-01-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The N-terminal Ala residue is modified with a
; OTHER INFORMATION: succinyl group; the C-terminal Phe residue is
; OTHER INFORMATION: modified with a nitroanilide group.
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-117-380B-2
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Query Match          66.7%; Score 4; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
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```
Qy      3 AAPF 6
        ||||
Db      1 AAPF 4
```

RESULT 4

US-09-935-744-1

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; Sequence 1, Application US/09935744
; Patent No. US20020137118A1
; GENERAL INFORMATION:
; APPLICANT: Inouye, Masayori
; APPLICANT: Shinde, Ujwal
; APPLICANT: Fu, Xuan
; TITLE OF INVENTION: Biologically Active Protein Folding Intermediates
; FILE REFERENCE: 266/223
; CURRENT APPLICATION NUMBER: US/09/935,744
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: The sequence is part of a synthetic peptide that is used
as a sub
; OTHER INFORMATION: strate for determining the activation time of a stable
crosslinke
; OTHER INFORMATION: d intermediate conformer.
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(4)
; OTHER INFORMATION: Sequence is preceded by N-succinyl and followed by p-
nitroanilide
US-09-935-744-1
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Query Match          66.7%; Score 4; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
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```
Qy      3 AAPF 6
        ||||
Db      1 AAPF 4
```

RESULT 5

US-10-373-794-3

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; Sequence 3, Application US/10373794
; Publication No. US20030152564A1
; GENERAL INFORMATION:
; APPLICANT: FRIDKIN, Matityahu
; APPLICANT: YAVIN, Eran
; TITLE OF INVENTION: ANTI-INFLAMMATORY PEPTIDES DERIVED FROM C-REACTIVE
PROTEIN
; FILE REFERENCE: FRIDKIN=3
; CURRENT APPLICATION NUMBER: US/10/373,794
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US/09/446,868
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: PCT/IL98/00302
; PRIOR FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: IL 121191
; PRIOR FILING DATE: 1997-06-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: The N-terminal Ala residue is modified with a succinyl
moiety and
; OTHER INFORMATION: the C-terminal Phe residue is modified with a
nitroanilide moiety
; OTHER INFORMATION: y.
US-10-373-794-3
```

```
Query Match          66.7%; Score 4; DB 12; Length 4;
```

Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AAPF 6

||||

Db 1 AAPF 4

RESULT 6

US-10-087-942-32

; Sequence 32, Application US/10087942

; Publication No. US20030165808A1

; GENERAL INFORMATION:

; APPLICANT: Haaland, Perry D.

; APPLICANT: Sherman, Douglas B.

; APPLICANT: Stewart II, Walter W.

; APPLICANT: Lloyd, Sheila A.

; APPLICANT: Campbell, Robert L.

; TITLE OF INVENTION: METHODS, APPARATUS AND COMPUTER PROGRAM PRODUCTS FOR

; TITLE OF INVENTION: FORMULATING CULTURE MEDIA

; FILE REFERENCE: P3250

; CURRENT APPLICATION NUMBER: US/10/087,942

; CURRENT FILING DATE: 2002-03-05

; PRIOR APPLICATION NUMBER: US/09/359,260

; PRIOR FILING DATE: 1999-07-22

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 32

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: hypothetical

; OTHER INFORMATION: peptide

US-10-087-942-32

Query Match 66.7%; Score 4; DB 12; Length 4;

Best Local Similarity 100.0%; Pred. No. 6.5e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAA 4

||||

Db 1 AAAA 4

RESULT 7

US-10-443-701-2

; Sequence 2, Application US/10443701

; Publication No. US20030199016A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Yuan

; TITLE OF INVENTION: REVERSE-PHASE HPLC ASSAY FOR PLASMINOGEN ACTIVATORS

; FILE REFERENCE: P1788R1

; CURRENT APPLICATION NUMBER: US/10/443,701

; CURRENT FILING DATE: 2003-05-21

; PRIOR APPLICATION NUMBER: US/09/703,695

; PRIOR FILING DATE: 2000-11-01

; PRIOR APPLICATION NUMBER: US 60/163,607
; PRIOR FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial Sequence.
US-10-443-701-2

Query Match 66.7%; Score 4; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAA 4
 ||||
Db 1 AAAA 4

RESULT 8

US-10-138-375-77

; Sequence 77, Application US/10138375

; Publication No. US20030208037A1

; GENERAL INFORMATION:

; APPLICANT: Zhang, Han-Zhong

; APPLICANT: Cai, Sui Xiong

; APPLICANT: Drewe, John A.

; APPLICANT: Yang, Wu

; TITLE OF INVENTION: No. US20030208037A1e1 Fluorescence Dyes and Their
Applications for Whole-Cell

; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases,
Proteases and

; TITLE OF INVENTION: Other Enzymes and the Use Thereof

; FILE REFERENCE: 1735.0030001

; CURRENT APPLICATION NUMBER: US/10/138,375

; CURRENT FILING DATE: 2002-05-06

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642

; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998

; NUMBER OF SEQ ID NOS: 139

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 77

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Peptide

US-10-138-375-77

Query Match 66.7%; Score 4; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAA 4

Db ||||
1 AAAA 4

RESULT 9

US-10-397-160-66

; Sequence 66, Application US/10397160
; Publication No. US20030232761A1
; GENERAL INFORMATION:
; APPLICANT: HINKE, SIMON A.
; APPLICANT: MANHART, SUSANNE
; APPLICANT: EHSES, JAN A.
; APPLICANT: MCINTOSH, CHRISTOPHER H.S.
; APPLICANT: DEMUTH, HANS-ULRICH
; APPLICANT: PEDERSON, RAYMOND A.
; TITLE OF INVENTION: NOVEL ANALOGUES OF GLUCOSE-DEPENDENT INSULINOTROPIC
; TITLE OF INVENTION: POLYPEPTIDE
; FILE REFERENCE: 20488/37
; CURRENT APPLICATION NUMBER: US/10/397,160
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/368,197
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: linker peptide
US-10-397-160-66

Query Match 66.7%; Score 4; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAA 4
 ||||
Db 1 AAAA 4

RESULT 10

US-10-090-624-33

; Sequence 33, Application US/10090624
; Publication No. US20020132335A1
; GENERAL INFORMATION:
; APPLICANT: TAKAKURA, Hikaru
; APPLICANT: MORISHITA, Mio
; APPLICANT: SHIMOJO, Tomoko
; APPLICANT: ASADA, Kiyozo
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
; FILE REFERENCE: TAKAKURA=6
; CURRENT APPLICATION NUMBER: US/10/090,624
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: 09/445,472

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; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 151969/1997
; PRIOR FILING DATE: 1997-06-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Residue 1 is modified by a succinyl group.
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Residue 4 is modified by a p-nitroaniline group.
US-10-090-624-33

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Query Match          66.7%; Score 4; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      3 AAPF 6
        ||||
Db      1 AAPF 4

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RESULT 11

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US-10-036-371-7
; Sequence 7, Application US/10036371
; Publication No. US20020141987A1
; GENERAL INFORMATION:
; APPLICANT: BJARNARSON, JON B.
; TITLE OF INVENTION: FISH SERINE PROTEINASES AND THEIR PHARMACEUTICAL AND
; TITLE OF INVENTION: COSMETIC USE
; FILE REFERENCE: 81691/284960
; CURRENT APPLICATION NUMBER: US/10/036,371
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/411,688
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 5086/99
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
US-10-036-371-7

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Query Match          66.7%; Score 4; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy 3 AAPF 6
|||
Db 1 AAPF 4

RESULT 12

US-10-040-655-10

; Sequence 10, Application US/10040655
; Publication No. US20020146805A1
; GENERAL INFORMATION:
; APPLICANT: Andrade-Gordon, Patricia
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jian-shen
; TITLE OF INVENTION: DNA encoding the novel human serine
; TITLE OF INVENTION: protease T
; FILE REFERENCE: ORT-1032
; CURRENT APPLICATION NUMBER: US/10/040,655
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide substrate
US-10-040-655-10

Query Match 66.7%; Score 4; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AAPF 6
|||
Db 1 AAPF 4

RESULT 13

US-10-033-526-1

; Sequence 1, Application US/10033526
; Publication No. US20020147999A1
; GENERAL INFORMATION:
; APPLICANT: Robert W. Mahley
; APPLICANT: Yadong Huang
; TITLE OF INVENTION: Methods of Treating Disorders Related to
; TITLE OF INVENTION: APOE
; FILE REFERENCE: UCAL217
; CURRENT APPLICATION NUMBER: US/10/033,526
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 60/245,737
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-033-526-1

Query Match 66.7%; Score 4; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAPF 6
|||
Db 1 AAPF 4

RESULT 14

US-10-133-912-21

; Sequence 21, Application US/10133912
; Publication No. US20020165358A1

; GENERAL INFORMATION:

; APPLICANT: Kinoshita, Masahiko
; Yamaguchi, Kyoji
; Goto, Masaaki
; Murakami, Akihiko
; Ueda, Masatsugu
; Higashio, Kanji
; Yamashita, Yasushi

; TITLE OF INVENTION: TCF MUTANT

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burgess, Ryan and Wayne
; STREET: 370 Lexington Avenue, Suite 2105
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 10017

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3 1/5 inch diskette
; COMPUTER: PC'S LIMITED SYSTEM 200
; OPERATING SYSTEM: WORD FOR WINDOWS
; SOFTWARE: MICROSOFT WINDOWS 98

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/133,912
; FILING DATE: 25-Apr-2002
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/700,519
; FILING DATE: 26-Aug-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Wayne, Milton J.
; REGISTRATION NUMBER: 17,906
; REFERENCE/DOCKET NUMBER: U-Wp-5240PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-683-8150
; TELEFAX: 212-532-4285

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4
; TYPE: AMINO ACID

; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-133-912-21

Query Match 66.7%; Score 4; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAA 4
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Db 1 AAAA 4

RESULT 15

US-10-041-006A-10

; Sequence 10, Application US/10041006A
; Publication No. US20020168754A1
; GENERAL INFORMATION:
; APPLICANT: Andrade-Gordon, Patricia
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jian-shen
; TITLE OF INVENTION: DNA encoding the novel human serine
; TITLE OF INVENTION: protease T
; FILE REFERENCE: ORT-1032
; CURRENT APPLICATION NUMBER: US/10/041,006A
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide substrate
US-10-041-006A-10

Query Match 66.7%; Score 4; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AAPF 6
|||
Db 1 AAPF 4

Search completed: December 30, 2003, 12:36:16
Job time : 30.4286 secs

OM protein - protein search, using sw model

Run on: December 30, 2003, 12:19:51 ; Search time 14.1429 Seconds
 (without alignments)
 40.799 Million cell updates/sec

Title: US-10-033-526-4
 Perfect score: 6
 Sequence: 1 AAAAPF 6

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 293

Minimum DB seq length: 4

Maximum DB seq length: 6

Post-processing: Listing first 45 summaries

Database : PIR_76:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	5	83.3	5	2	JS0319	subesophageal gang
2	3	50.0	6	2	B60110	repetitive protein
3	2	33.3	4	2	A34626	RPCH-related neuro
4	2	33.3	5	2	B41225	copper resistance
5	2	33.3	5	2	B60274	major protein anti
6	2	33.3	5	2	PS0324	ribulose-bisphosph
7	2	33.3	5	2	S55237	zinc-binding prote
8	2	33.3	5	2	G37196	bradykinin-potenti
9	2	33.3	5	2	S11127	phosphoprotein, bo
10	2	33.3	6	2	S66195	alcohol dehydrogen
11	2	33.3	6	2	A61049	halo-toxin - Pseud
12	2	33.3	6	2	C22565	R-phycoerythrin be
13	2	33.3	6	2	A43766	28K ubiquitin-immu

14	2	33.3	6	2	B27696	contraction-inhibi
15	2	33.3	6	2	I51317	bHLH transcription
16	2	33.3	6	2	PT0280	Ig heavy chain CRD
17	2	33.3	6	2	PT0616	T-cell receptor be
18	2	33.3	6	4	S15596	orf 3 rara 5'-regi
19	1	16.7	4	1	ECXAA	antho-RFamide neur
20	1	16.7	4	2	S18401	thyroglobulin - do
21	1	16.7	4	2	A02147	phagocytosis-stimu
22	1	16.7	4	2	A32039	tyrosine-melanocyt
23	1	16.7	4	2	ECNK	cardioexcitatory n
24	1	16.7	4	2	PL0140	carbon-monoxide de
25	1	16.7	4	2	PL0146	carbon-monoxide de
26	1	16.7	4	2	A48360	gamma subunit of P
27	1	16.7	4	2	S43014	hypothetical prote
28	1	16.7	4	2	D41654	hypothetical prote
29	1	16.7	4	2	S53508	starvation-induced
30	1	16.7	4	2	S17255	ribosomal protein
31	1	16.7	4	2	A27897	glucan 1,4-alpha-g
32	1	16.7	4	2	JQ1273	neuropeptide Antho
33	1	16.7	4	2	A35779	neuropeptide Antho
34	1	16.7	4	2	A25844	autho-RF amide neu
35	1	16.7	4	2	A60418	FMRFamide - polych
36	1	16.7	4	2	A32480	achatin-I - giant
37	1	16.7	4	2	I51049	metallothionein-A
38	1	16.7	4	2	S39390	myosin-light-chain
39	1	16.7	4	2	I61883	protamine P1 - ora
40	1	16.7	4	2	PT0240	Ig heavy chain CRD
41	1	16.7	4	2	PT0271	Ig heavy chain CRD
42	1	16.7	4	2	S43959	Ig mu chain V regi
43	1	16.7	4	2	I54357	schwannomin - mous
44	1	16.7	4	2	PT0696	T-cell receptor be
45	1	16.7	4	2	PT0645	T-cell receptor be

ALIGNMENTS

RESULT 1

JS0319

subesophageal ganglion pentapeptide - house cricket

C;Species: Acheta domesticus (house cricket)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000

C;Accession: JS0319

R;Wicker, C.; Wicker, C.

Comp. Biochem. Physiol. C 88, 185-187, 1987

A;Title: Isolation and structure of a peptide isolated from the subesophageal ganglion of Acheta domesticus (orthoptera).

A;Reference number: JS0319

A;Accession: JS0319

A;Molecule type: protein

A;Residues: 1-5 <WIC>

Query Match 83.3%; Score 5; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2 AAAPF 6

Db |||||
 1 AAAPF 5

RESULT 2

B60110

repetitive protein antigen 61 - Trypanosoma cruzi (fragment)

C;Species: Trypanosoma cruzi

C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 18-Jun-1993

C;Accession: B60110

R;Hoft, D.F.; Kim, K.S.; Otsu, K.; Moser, D.R.; Yost, W.J.; Blumin, J.H.;
Donelson, J.E.; Kirchhoff, L.V.

Infect. Immun. 57, 1959-1967, 1989

A;Title: Trypanosoma cruzi expresses diverse repetitive protein antigens.

A;Reference number: A60110; MUID:89277508; PMID:2659529

A;Accession: B60110

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-6 <HOF>

A;Note: this is an example of a five residue tandem repeat from this protein;
the actual protein sequence is not given in the paper

C;Keywords: tandem repeat

Query Match 50.0%; Score 3; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AAP 5

Db |||
 1 AAP 3

RESULT 3

A34626

RPCH-related neuropeptide - ferruginous spindle

C;Species: Fusinus ferrugineus (ferruginous spindle)

C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993

C;Accession: A34626

R;Kuroki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.;
Minamitake, Y.; Muneoka, Y.

Biochem. Biophys. Res. Commun. 167, 273-279, 1990

A;Title: A molluscan neuropeptide related to the crustacean hormone, RPCH.

A;Reference number: A34626; MUID:90179762; PMID:2310394

A;Accession: A34626

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-4 <KUR>

C;Keywords: neuropeptide

Query Match 33.3%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AP 5

Db ||
 1 AP 2

RESULT 4

B41225

copper resistance protein B - *Pseudomonas syringae* pv. tomato (fragment)

C;Species: *Pseudomonas syringae* pv. tomato

C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993

C;Accession: B41225

R;Cha, J.S.; Cooksey, D.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991

A;Title: Copper resistance in *Pseudomonas syringae* mediated by periplasmic and outer membrane proteins.

A;Reference number: A41225; MUID:92020961; PMID:1924351

A;Accession: B41225

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-5 <CHA>

Query Match 33.3%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AA 2
||
Db 3 AA 4

RESULT 5

B60274

major protein antigen MPT32 - *Mycobacterium tuberculosis* (fragment)

C;Species: *Mycobacterium tuberculosis*

C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993

C;Accession: B60274

R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.

Infect. Immun. 59, 372-382, 1991

A;Title: Isolation and partial characterization of major protein antigens in the culture fluid of *Mycobacterium tuberculosis*.

A;Reference number: A60274; MUID:91099989; PMID:1898899

A;Accession: B60274

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-5 <NAG>

Query Match 33.3%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AP 5
||
Db 3 AP 4

RESULT 6

PS0324

ribulose-bisphosphate carboxylase activase III - rice (strain Nihonbare) (fragment)

C;Species: *Oryza sativa* (rice)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 02-Jul-1998

C;Accession: PS0324
R;Tsugita, A.
submitted to JIPID, April 1993
A;Reference number: PS0206
A;Accession: PS0324
A;Molecule type: protein
A;Residues: 1-5 <TSU>
A;Experimental source: leaf, chlorophyll

Query Match 33.3%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AP 5
||
Db 3 AP 4

RESULT 7

S55237

zinc-binding protein ZBP14 - maize (fragment)

C;Species: Zea mays (maize)

C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999

C;Accession: S55237

R;Robinson, K.; Jones, D.; Howell, S.; Soneji, Y.; Martin, S.; Aitken, A.
Biochem. J. 307, 267-272, 1995

A;Title: Expression and characterization of maize ZBP14, a member of a new family of zinc-binding proteins.

A;Reference number: S55237; MUID:95234046; PMID:7717986

A;Accession: S55237

A;Molecule type: protein

A;Residues: 1-5 <ROB>

Query Match 33.3%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AA 2
||
Db 2 AA 3

RESULT 8

G37196

bradykinin-potentiating peptide 7 - island jararaca

C;Species: Bothrops insularis (island jararaca)

C;Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994

C;Accession: G37196

R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990

A;Title: Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.

A;Reference number: A37196; MUID:90351557; PMID:2386615

A;Accession: G37196

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-5 <CIN>

C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 33.3%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AP 5
||
Db 4 AP 5

RESULT 9

S11127

phosphoprotein, bone - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Mar-2000

C;Accession: S11127; S11128

R;Mikuni-Takagaki, Y.; Glimcher, M.J.

Biochem. J. 268, 585-591, 1990

A;Title: Post-translational processing of chicken bone phosphoproteins.
Identification of the bone phosphoproteins of embryonic tibia.

A;Reference number: S11127; MUID:90303246; PMID:2363696

A;Accession: S11127

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-5 <MIK1>

A;Accession: S11128

A;Status: preliminary

A;Molecule type: protein

A;Residues: 'X',2-5 <MIK2>

C;Keywords: phosphoprotein

Query Match 33.3%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AP 5
||
Db 1 AP 2

RESULT 10

S66195

alcohol dehydrogenase (EC 1.1.1.1) class III low affinity form - cod (Gadus sp.)
(fragment)

C;Species: Gadus sp. (cod)

C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 12-Jun-1998

C;Accession: S66195

R;Hjelmqvist, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.;

Hendrickson, R.C.; Michel, H.; Shabanowitz, J.; Hunt, D.F.; Joernvall, H.

FEBS Lett. 367, 237-240, 1995

A;Title: Multiplicity of N-terminal structures of medium-chain alcohol
dehydrogenases. Mass-spectrometric analysis of plant, lower vertebrate and
higher vertebrate class I, II, and III forms of the enzyme.

A;Reference number: S66191; MUID:95331382; PMID:7607314

A;Accession: S66195

A;Molecule type: protein
A;Residues: 1-6 <HJE>
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 33.3%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AA 2
||
Db 1 AA 2

RESULT 11

A61049
halo-toxin - *Pseudomonas syringae* pv. *mori*
C;Species: *Pseudomonas syringae* pv. *mori*
A;Note: host mulberry tree
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 21-Jan-1997
C;Accession: A61049
R;Kajimoto, T.; Yokomizo, K.; Yahiro, K.; Umeda, T.; Shoji, S.; Kubota, Y.;
Shibata, M.; Takahashi, K.; Nohara, T.
Chem. Lett. 00, 679-680, 1989
A;Title: Structure of halo-toxin produced by phytopathogenic bacterium,
Pseudomonas syringae pv. *mori*.
A;Reference number: A61049
A;Accession: A61049
A;Molecule type: protein
A;Residues: 1-6 <KAJ>
A;Note: sequence confirmed by synthesis
C;Comment: This toxin is one of the etiological agents of halo bright disease in
mulberry tress.
C;Keywords: toxin

Query Match 33.3%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PF 6
||
Db 1 PF 2

RESULT 12

C22565
R-phycoerythrin beta-1 chain - red alga (*Gastroclonium coulteri*) (fragment)
C;Species: *Gastroclonium coulteri*
C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C;Accession: C22565
R;Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A;Reference number: A22565; MUID:85182601; PMID:3886644
A;Accession: C22565
A;Molecule type: protein
A;Residues: 1-6 <KLO>

Query Match 33.3%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AA 2
||
Db 2 AA 3

RESULT 13

A43766

28K ubiquitin-immunoreactive protein - inky cap (*Coprinus cinereus*) (fragment)

C;Species: *Coprinus cinereus*

C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 30-Sep-1993

C;Accession: A43766

R;Kanda, T.; Inoue, M.; Akiyama, M.

Biochimie 72, 355-359, 1990

A;Title: Purification and characterization of an ubiquitin-immuno-reactive protein localized in the cap of young basidiocarp in the basidiomycete *Coprinus cinereus*.

A;Reference number: A43766; MUID:91002724; PMID:1698461

A;Accession: A43766

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-6 <KAN>

Query Match 33.3%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AP 5
||
Db 1 AP 2

RESULT 14

B27696

contraction-inhibiting peptide II - blue mussel

C;Species: *Mytilus edulis* (blue mussel)

C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 08-Dec-1995

C;Accession: B27696

R;Hirata, T.; Kubota, I.; Iwasawa, N.; Takabatake, I.; Ikeda, T.; Muneoka, Y.
Biochem. Biophys. Res. Commun. 152, 1376-1382, 1988

A;Title: Structures and actions of *Mytilus* inhibitory peptides.

A;Reference number: A90142; MUID:88240357; PMID:3377776

A;Accession: B27696

A;Molecule type: protein

A;Residues: 1-6 <HIR>

C;Keywords: amidated carboxyl end

F;6/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 33.3%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AP 5

Db ||
 2 AP 3

RESULT 15

I51317

bHLH transcription factor inhibitor - African clawed frog (fragment)

C;Species: Xenopus laevis (African clawed frog)

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C;Accession: I51317

R;Zhang, H.; Reynaud, S.; Kloc, M.; Etkin, L.D.; Spohr, G.

Mech. Dev. 50, 119-130, 1995

A;Title: Id gene activity during Xenopus embryogenesis.

A;Reference number: I51316; MUID:95344988; PMID:7619724

A;Accession: I51317

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-6 <ZHA>

A;Cross-references: GB:S79038; NID:g1042006; PIDN:AAD14294.1; PID:g4261994

C;Genetics:

A;Gene: XidIb

Query Match 33.3%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PF 6

||

Db 5 PF 6

Search completed: December 30, 2003, 12:24:28

Job time : 15.1429 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 12:16:41 ; Search time 9.85714 Seconds
(without alignments)
28.625 Million cell updates/sec

Title: US-10-033-526-4
Perfect score: 6
Sequence: 1 AAAAPF 6

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 47

Minimum DB seq length: 4

Maximum DB seq length: 6

Post-processing: Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	5	83.3	5	1	SUGA_ACHDO	P19991 acheta dome
2	2	33.3	5	1	BPP7_BOTIN	P30425 bothrops in
3	2	33.3	6	1	CIP2_MYTED	P13737 mytilus edu
4	1	16.7	4	1	ACH1_ACHFU	P35904 achatina fu
5	1	16.7	4	1	DCML_PSECH	P19916 pseudomonas
6	1	16.7	4	1	DCMS_PSECH	P19918 pseudomonas
7	1	16.7	4	1	FAR3_HIRME	P42562 hirudo medi
8	1	16.7	4	1	FAR4_HIRME	P42563 hirudo medi
9	1	16.7	4	1	FFKA_ANTEL	P58705 anthopleura
10	1	16.7	4	1	FLRF_HIRME	P42561 hirudo medi
11	1	16.7	4	1	FLRN_ANTEL	P58707 anthopleura
12	1	16.7	4	1	FMRF_MACNI	P01162 macrocallis
13	1	16.7	4	1	FYRI_ANTEL	P58706 anthopleura
14	1	16.7	4	1	OCP1_OCTMI	P58648 octopus min
15	1	16.7	4	1	RM01_YEAST	P36515 saccharomyc
16	1	16.7	4	1	TUFT_HUMAN	P01858 homo sapien
17	1	16.7	5	1	AL14_CARMA	P81817 carcinus ma

18	1	16.7	5	1	BIOB_CITFR	P12997 citrobacter
19	1	16.7	5	1	EI03_LITRU	P82099 litoria rub
20	1	16.7	5	1	EI04_LITRU	P82100 litoria rub
21	1	16.7	5	1	FARP_ARTTR	P41853 artioposthi
22	1	16.7	5	1	PAP2_PARMA	P81864 pardachirus
23	1	16.7	5	1	PRCT_PERAM	P01373 periplaneta
24	1	16.7	5	1	RE11_LITRU	P82070 litoria rub
25	1	16.7	5	1	RE21_LITRU	P82071 litoria rub
26	1	16.7	5	1	RE31_LITRU	P82072 litoria rub
27	1	16.7	5	1	RE32_LITRU	P82073 litoria rub
28	1	16.7	5	1	TPIS_CANFA	P54714 canis famil
29	1	16.7	5	1	UC22_MAIZE	P80628 zea mays (m
30	1	16.7	6	1	CIP1_MYTED	P13736 mytilus edu
31	1	16.7	6	1	EI01_LITRU	P82096 litoria rub
32	1	16.7	6	1	FARP_MONEX	P41966 moniezia ex
33	1	16.7	6	1	LOK1_LOCFMI	P41491 locusta mig
34	1	16.7	6	1	OVM_LEPDE	P42985 leptinotars
35	1	16.7	6	1	TMOF_SARBU	P41495 sarcophaga
36	1	16.7	6	1	TRPI_PSEPU	P36414 pseudomonas
37	1	16.7	6	1	UN06_CLOPA	P81351 clostridium
38	1	16.7	6	1	VP19_HSV1K	P23210 herpes simp
39	0	0.0	4	1	EOS1_HUMAN	P02731 homo sapien
40	0	0.0	4	1	OCP3_OCTMI	P58649 octopus min
41	0	0.0	5	1	BIOA_CITFR	P13071 citrobacter
42	0	0.0	5	1	PSK_DAUCA	P58261 daucus caro
43	0	0.0	5	1	TRM3_ECOLI	P13973 escherichia
44	0	0.0	5	1	UF01_MOUSE	P38639 mus musculu
45	0	0.0	5	1	UXA4_CHLTR	P38005 chlamydia t

ALIGNMENTS

RESULT 1

SUGA_ACHDO

ID SUGA_ACHDO STANDARD; PRT; 5 AA.
 AC P19991;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Suboesophageal ganglion pentapeptide.
 OS Acheta domesticus (House cricket).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
 OC Acheta.
 OX NCBI_TaxID=6997;
 RN [1]
 RP SEQUENCE.
 RA Wicker C., Wicker C.;
 RT "Isolation and structure of a peptide isolated from the
 RT suboesophageal ganglion of Acheta domesticus (orthoptera).";
 RL Comp. Biochem. Physiol. 88C:185-187(1987).
 CC -!- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBOESOPHAGEAL
 CC GANGLIA.
 DR PIR; JS0319; JS0319.
 SQ SEQUENCE 5 AA; 476 MW; 69D76DDDDDB00000 CRC64;

Query Match 83.3%; Score 5; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAAPF 6
|||
Db 1 AAAPF 5

RESULT 2

BPP7_BOTIN

ID BPP7_BOTIN STANDARD; PRT; 5 AA.
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom."
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; G37196; G37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AP 5
||
Db 4 AP 5

RESULT 3

CIP2_MYTED

ID CIP2_MYTED STANDARD; PRT; 6 AA.
AC P13737;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Contraction-inhibiting peptide II (MIP II).

OS Mytilus edulis (Blue mussel).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
 OC Mytiloidea; Mytilidae; Mytilus.
 OX NCBI_TaxID=6550;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pedal ganglion;
 RX MEDLINE=88240357; PubMed=3377776;
 RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
 RT "Structures and actions of Mytilus inhibitory peptides."
 RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
 CC -!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
 CC MUSCLES.
 CC -!- SIMILARITY: TO MIP I.
 DR PIR; B27696; B27696.
 KW Hormone; Amidation.
 FT MOD_RES 6 6 AMIDATION.
 SQ SEQUENCE 6 AA; 621 MW; 72C9C6876DD81000 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AP 5
 ||
 Db 2 AP 3

RESULT 4

ACH1_ACHFUFU

ID ACH1_ACHFUFU STANDARD; PRT; 4 AA.
 AC P35904;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Achatin-I.
 OS Achatina fulica (Giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
 RC STRAIN=Ferussac; TISSUE=Ganglion;
 RX MEDLINE=89273551; PubMed=2597281;
 RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
 RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
 RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
 RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
 RT fulica Ferussac containing a D-amino acid residue."
 RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
 RN [2]
 RP CHARACTERIZATION.
 RC STRAIN=Ferussac; TISSUE=Heart atrium;
 RX MEDLINE=91264856; PubMed=1675568;
 RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
 RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
 RT "Purification of achatin-I from the atria of the African giant snail,

RT Achatina fulica, and its possible function.";
 RL Biochem. Biophys. Res. Commun. 177:847-853(1991).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=93014529; PubMed=1399265;
 RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
 RA Iwashita T., Nomoto K.;
 RT "Crystal structure and molecular conformation of achatin-I
 RT (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
 RT D-amino acid residue.";
 RL Int. J. Pept. Protein Res. 39:258-264(1992).
 CC -!- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY
 CC AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY
 CC NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE
 CC HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.
 DR PIR; A32480; A32480.
 KW Hormone; D-amino acid.
 FT MOD_RES 2 2 D-PHENYLALANINE.
 SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;

Query Match 16.7%; Score 1; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 F 6
 |
 Db 2 F 2

RESULT 5

DCML_PSECH

ID DCML_PSECH STANDARD; PRT; 4 AA.
 AC P19916;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO
 DE dehydrogenase subunit L) (CO-DH L) (Fragment).
 GN CUTL.
 OS Pseudomonas carboxydohydrogena.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae.
 OX NCBI_TaxID=290;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90055678; PubMed=2818128;
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 RT carboxydotrophic bacteria.";
 RL Arch. Microbiol. 152:335-341(1989).
 CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
 CC dioxide.
 CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
 CC acceptor.
 CC -!- COFACTOR: Molybdenum (molybdopterin).
 CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 CC SMALL.

DR PIR; PL0140; PL0140.
KW Oxidoreductase; Molybdenum.
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;

Query Match 16.7%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 P 5
|
Db 4 P 4

RESULT 6

DCMS_PSECH

ID DCMS_PSECH STANDARD; PRT; 4 AA.
AC P19918;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO
dehydrogenase subunit S) (CO-DH S) (Fragment).
GN CUTS.
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae.
OX NCBI_TaxID=290;
RN [1]
RP SEQUENCE.
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
RT carboxydotrophic bacteria."
RL Arch. Microbiol. 152:335-341(1989).
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
CC dioxide.
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
CC acceptor.
CC -!- COFACTOR: BINDS TWO 2FE-2S CLUSTERS.
CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC SMALL.
DR PIR; PL0146; PL0146.
KW Oxidoreductase; Metal-binding; Iron-sulfur; Iron; 2Fe-2S.
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 420 MW; 6DD33DD6F0000000 CRC64;

Query Match 16.7%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 A 1
|
Db 2 A 2

RESULT 7

FAR3_HIRME

ID FAR3_HIRME STANDARD; PRT; 4 AA.
 AC P42562;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide YLRF-amide.
 OS Hirudo medicinalis (Medicinal leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92195954; PubMed=1686933;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech."
 RL Peptides 12:897-908(1991).
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 4 4 AMIDATION.
 SQ SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;

Query Match 16.7%; Score 1; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 F 6
 |
 Db 4 F 4

RESULT 8

FAR4_HIRME

ID FAR4_HIRME STANDARD; PRT; 4 AA.
 AC P42563;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide YMRP-amide.
 OS Hirudo medicinalis (Medicinal leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92195954; PubMed=1686933;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech."
 RL Peptides 12:897-908(1991).
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 4 4 AMIDATION.
 SQ SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;

Query Match 16.7%; Score 1; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 F 6
|
Db 4 F 4

RESULT 9

FFKA_ANTEL

ID FFKA_ANTEL STANDARD; PRT; 4 AA.
AC P58705;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Antho-KAamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynantheae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE.
RX MEDLINE=92028852; PubMed=1681803;
RA Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
RT "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a
RT novel neuropeptide from sea anemones."
RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
RN [2]
RP FUNCTION.
RX MEDLINE=93391436; PubMed=8397415;
RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
RT inhibitory neuropeptides, Antho-KAamide and Antho-RIamide."
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Neuron-specific.
DR PIR; JQ1273; JQ1273.
KW Neuropeptide; Amidation.
FT MOD_RES 1 1 L-3-PHENYLLACTYL.
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 512 MW; 6DD339C9A0000000 CRC64;

Query Match 16.7%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 F 6
|
Db 1 F 1

RESULT 10

FLRF_HIRME

ID FLRF_HIRME STANDARD; PRT; 4 AA.

AC P42561;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FLRFamide.
 OS *Hirudo medicinalis* (Medicinal leech), and
 OS *Helisoma trivolvis* (Snail).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Arynchobdellida; Hirudiniformes; Hirudinidae; *Hirudo*.
 OX NCBI_TaxID=6421, 27815;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=*H.medicinalis*;
 RX MEDLINE=92195954; PubMed=1686933;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech.";
 RL Peptides 12:897-908(1991).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=*H.trivolvis*; TISSUE=Kidney;
 RX MEDLINE=94286417; PubMed=7912428;
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
 RT "FMRFamide-related peptides from the kidney of the snail, *Helisoma*
 RT *trivolvis*.";
 RL Peptides 15:31-36(1994).
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 4 4 AMIDATION.
 SQ SEQUENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;

Query Match 16.7%; Score 1; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 F 6
 |
 Db 1 F 1

RESULT 11

FLRN_ANTEL

ID FLRN_ANTEL STANDARD; PRT; 4 AA.
 AC P58707;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Antho-RNamide.
 OS *Anthopleura elegantissima* (Sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nynanthaeae; Actiniidae; *Anthopleura*.
 OX NCBI_TaxID=6110;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RX MEDLINE=90319122; PubMed=1973541;
 RA Grimmlikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
 RA Reinscheid R.K., Nothacker H.-P., Staley A.L.;

RT "Isolation of L-3-phenyllactyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea
 RT anemone neuropeptide containing an unusual amino-terminal blocking
 RT group.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Neuron-specific.
 CC -!- MASS SPECTROMETRY: MW=549.3; METHOD=FAB.
 DR PIR; A35779; A35779.
 KW Neuropeptide; Amidation.
 FT MOD_RES 1 1 L-3-PHENYLLACTYL.
 FT MOD_RES 4 4 AMIDATION.
 SQ SEQUENCE 4 AA; 549 MW; 64540729A0000000 CRC64;

Query Match 16.7%; Score 1; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 F 6
 |
 Db 1 F 1

RESULT 12

FMRF_MACNI

ID FMRF_MACNI STANDARD; PRT; 4 AA.
 AC P01162;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE FMRFamide (Peak C) (Cardioexcitatory neuropeptide).
 OS Macrocallista nimbosa (Sun-ray clam),
 OS Nereis virens (Sandworm),
 OS Hirudo medicinalis (Medicinal leech), and
 OS Helisoma trivolvis (Snail).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;
 OC Veneroidea; Veneridae; Macrocallista.
 OX NCBI_TaxID=6594, 6353, 6421, 27815;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC SPECIES=M.nimbosa; TISSUE=Cerebral pedal, and Visceral ganglion;
 RX MEDLINE=77215956; PubMed=877582;
 RA Price D.A., Greenberg M.J.;
 RT "Structure of a molluscan cardioexcitatory neuropeptide.";
 RL Science 197:670-671(1977).
 RN [2]
 RP SEQUENCE, AND CHARACTERIZATION.
 RC SPECIES=M.nimbosa; TISSUE=Ganglion;
 RX MEDLINE=78012038; PubMed=909875;
 RA Price D.A., Greenberg M.J.;
 RT "Purification and characterization of a cardioexcitatory neuropeptide
 RT from the central ganglia of a bivalve mollusc.";
 RL Prep. Biochem. 7:261-281(1977).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=N.virens;
 RX MEDLINE=90259866; PubMed=2342992;
 RA Krajniak K.G., Price D.A.;

RT "Authentic FMRFamide is present in the polychaete Nereis virens.";
 RL Peptides 11:75-77(1990).
 RN [4]
 RP SEQUENCE.
 RC SPECIES=H.medicinalis;
 RX MEDLINE=92195954; PubMed=1686933;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech.";
 RL Peptides 12:897-908(1991).
 RN [5]
 RP SEQUENCE.
 RC SPECIES=H.trivolvus; TISSUE=Kidney;
 RX MEDLINE=94286417; PubMed=7912428;
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
 RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
 RT trivolvus.";
 RL Peptides 15:31-36(1994).
 CC -!- FUNCTION: MYOACTIVE; CARDIOEXCITATORY SUBSTANCE. PHARMACOLOGICAL
 CC ACTIVITIES INCLUDE AUGMENTATION, INDUCTION, AND REGULARIZATION OF
 CC CARDIAC CONTRACTION.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 DR PIR; A01426; ECKN.
 DR PIR; A60418; A60418.
 KW Neuropeptide; Amidation.
 FT MOD_RES 4 4 AMIDATION.
 SQ SEQUENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;

Query Match 16.7%; Score 1; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 F 6
 |
 Db 1 F 1

RESULT 13

FYRI_ ANTEL
 ID FYRI_ ANTEL STANDARD; PRT; 4 AA.
 AC P58706;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Antho-RIamide I [Contains: Antho-RIamide II].
 OS Anthopleura elegantissima (Sea anemone).
 OC Eukaryota; Metazoa; Chidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nynanthaeae; Actiniidae; Anthopleura.
 OX NCBI_TaxID=6110;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92270459; PubMed=1821096;
 RA Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D.,
 RA Grimmelikhuijzen C.J.P.;
 RT "Isolation of two novel neuropeptides from sea anemones: the unusual,
 RT biologically active L-3-phenyllactyl-Tyr-Arg-Ile-NH2 and its
 RT des-phenyllactyl fragment Tyr-Arg-Ile-NH2.";

RL Peptides 12:1165-1173(1991).
 RN [2]
 RP FUNCTION.
 RX MEDLINE=93391436; PubMed=8397415;
 RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
 RT "The expansion behaviour of sea anemones may be coordinated by two
 RT inhibitory neuropeptides, Antho-KAamide and Antho-RIamide.";
 RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
 CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle
 CC groups. May be involved in the expansion phase of feeding
 CC behaviour in sea anemones.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Neuron-specific.
 KW Neuropeptide; Amidation.
 FT CHAIN 1 4 ANTHO-RIAMIDE I.
 FT CHAIN 2 4 ANTHO-RIAMIDE II.
 FT MOD_RES 1 1 L-3-PHENYLLACTYL.
 FT MOD_RES 4 4 AMIDATION.
 SQ SEQUENCE 4 AA; 598 MW; 60441B59A0000000 CRC64;

Query Match 16.7%; Score 1; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 F 6
 |
 Db 1 F 1

RESULT 14

OCP1_OCTMI
 ID OCP1_OCTMI STANDARD; PRT; 4 AA.
 AC P58648;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cardioactive peptides Ocp-1/Ocp-2.
 OS Octopus minor (Octopus).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
 OX NCBI_TaxID=89766;
 RN [1]
 RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
 RC TISSUE=Brain;
 RX MEDLINE=20336815; PubMed=10876044;
 RA Iwakoshi E., Hisada M., Minakata H.;
 RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
 RT Octopus minor.";
 RL Peptides 21:623-630(2000).
 CC -!- FUNCTION: Cardioactive; has both positive chronotropic and
 CC inotropic effects on the heart. Ocp-2 is a 1000 time less
 CC active than Ocp-1.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PTM: Ocp-2 has L-Phe instead of D-Phe.
 CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
 KW Hormone; D-amino acid.
 FT MOD_RES 2 2 D-PHENYLALANINE.

SQ SEQUENCE 4 AA; 394 MW; 6AA879C810000000 CRC64;

Query Match 16.7%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 F 6
|
Db 2 F 2

RESULT 15

RM01_YEAST

ID RM01_YEAST STANDARD; PRT; 4 AA.
AC P36515;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Mitochondrial 60S ribosomal protein L1 (YmL1) (Fragment).
GN MRPL1.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RX MEDLINE=91285106; PubMed=2060626;
RA Grohmann L., Graack H.-R., Kruft V., Choli T., Goldschmidt-Reisin S.,
RA Kitakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal
RT subunit from yeast mitochondria."
RL FEBS Lett. 284:51-56(1991).
DR PIR; S17255; S17255.
DR SGD; L0002681; MRPL1.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000 CRC64;

Query Match 16.7%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 P 5
|
Db 4 P 4

Search completed: December 30, 2003, 12:23:41
Job time : 10.8571 secs

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: December 30, 2003, 12:20:27 ; Search time 34.2857 Seconds
(without alignments)
45.159 Million cell updates/sec

```
Title:      US-10-033-526-4
Perfect score: 6
Sequence:   1 AAAAPF 6
```

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 7

```
Minimum DB seq length: 4
Maximum DB seq length: 6
```

Post-processing: Listing first 45 summaries

```
Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
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1	1	16.7	5	10	Q99007	Q99007 hordeum vul
2	1	16.7	5	13	P83308	P83308 gallus gall
3	1	16.7	6	10	P82181	P82181 spinacia ol
4	1	16.7	6	10	P82182	P82182 spinacia ol
5	0	0.0	4	11	Q08433	Q08433 rattus sp.
6	0	0.0	5	2	P83073	P83073 bacillus ce
7	0	0.0	6	10	P82541	P82541 spinacia ol

ALIGNMENTS

RESULT 1

Q99007

ID Q99007 PRELIMINARY; PRT; 5 AA.
AC Q99007;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Alpha amylase (Fragment).
GN AMY1 GENE.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91329704; PubMed=1831055;
RA Jacobsen J.V., Close T.J.;
RT "Control of transient expression of chimaeric genes by gibberellic
RT acid and abscisic acid in protoplasts prepared from mature barley
RT aleurone layers."
RL Plant Mol. Biol. 16:713-721(1991).
DR EMBL; X54643; CAA38455.1; -.
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;

Query Match 16.7%; Score 1; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 A 1
Db	2 A 2

RESULT 2

P83308

ID P83308 PRELIMINARY; PRT; 5 AA.
AC P83308;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE FMRFamide-like neuropeptide (LPLRF-amide).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Brain;
 RX PubMed=6137771;
 RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
 RT "A novel active pentapeptide from chicken brain identified by
 RT antibodies to FMRFamide.";
 RL Nature 305:328-330(1983).
 CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide.
 SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 16.7%; Score 1; DB 13; Length 5;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 P 5
 |
 Db 2 P 2

RESULT 3

P82181

ID P82181 PRELIMINARY; PRT; 6 AA.
 AC P82181;
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Chloroplast 50S ribosomal protein L10 beta (Fragment).
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. ALWARO; TISSUE=Leaf;
 RX MEDLINE=20435798; PubMed=10874046;
 RA Yamaguchi K., Subramanian A.R.;
 RT "The plastid ribosomal proteins. Identification of all the proteins in
 RT the 50 S subunit of an organelle ribosome (chloroplast).";
 RL J. Biol. Chem. 275:28466-28482(2000).
 CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
 CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro; IPR001790; Ribosomal_L10.
 DR InterPro; IPR002363; Ribosomal_L10eub.
 DR Pfam; PF00466; Ribosomal_L10; PARTIAL.
 DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.

FT NON_TER 6 6
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 16.7%; Score 1; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 1 A 1

RESULT 4

P82182

ID P82182 PRELIMINARY; PRT; 6 AA.
AC P82182;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Chloroplast 50S ribosomal protein L10 gamma (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. ALWARO; TISSUE=Leaf;
RX MEDLINE=20435798; PubMed=10874046;
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro; IPR001790; Ribosomal_L10.
DR InterPro; IPR002363; Ribosomal_L10eub.
DR Pfam; PF00466; Ribosomal_L10; PARTIAL.
DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 16.7%; Score 1; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 1 A 1

RESULT 5

Q08433

ID Q08433 PRELIMINARY; PRT; 4 AA.
AC Q08433;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Bilirubin UDP-glucuronosyltransferase (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gunn;
RX MEDLINE=91282758; PubMed=1840486;
RA Sato H., Aono S., Kashiwamata S., Koiwai O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
RT hyperbilirubinemic Gunn rat.";
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
DR EMBL; S38636; AAB19259.1; -.
KW Transferase.
FT NON_TER 1 1
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 0.0%; Score 0; DB 11; Length 4;
Best Local Similarity 0.0%; Pred. No. 8.3e+05;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 A 1

Db 1 N 1

RESULT 6

P83073

ID P83073 PRELIMINARY; PRT; 5 AA.
AC P83073;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE 88 kDa protein (Fragment).
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE.
RC STRAIN=NCIMB 11796;
RA Browne N., Dowds B.C.A.;
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;

Query Match 0.0%; Score 0; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 8.3e+05;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 A 1

Db

1 M 1

RESULT 7

P82541

ID P82541 PRELIMINARY; PRT; 6 AA.
AC P82541;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Chloroplast 30S ribosomal protein S19 beta (Fragment).
OS Spinacia oleracea (Spinach).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC STRAIN=cv. ALWARO; TISSUE=Leaf;
RX MEDLINE=20435797; PubMed=10874039;
RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
the small subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 37:28455-28465(2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.
CC -!- MASS SPECTROMETRY: MW=10495; METHOD=MALDI.
CC -!- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PI. S19 BETA
FORM IS THE MINOR BASIC FORM.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 KDA.
CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro; IPR002222; Ribosomal_S19.
DR Pfam; PF00203; Ribosomal_S19; PARTIAL.
DR PRINTS; PR00975; RIBOSOMALS19; PARTIAL.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;

Query Match 0.0%; Score 0; DB 10; Length 6;
Best Local Similarity 0.0%; Pred. No. 8.3e+05;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 A 1

Db 1 T 1

Search completed: December 30, 2003, 12:26:00
Job time : 35.2857 secs